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(54) Title: TREATMENT OF NEURODEGENERATIVE DISEASES

(57) Abstract: The present invention relates to the uses of FADS2 interacting molecules, especially FADS2 inhibitors, for the preparation of a medicament for the treatment of neurodegenerative diseases, specially Alzheimer's disease.

Treatment of Neurodegenerative Diseases

The present invention relates to protein complexes of the APP-processing pathway comprising the FADS2 protein as well as to the use of inhibitors of these complexes as well as of FADS2 in the treatment of neurodegenerative diseases.

Alzheimer's disease is a chronic condition that affects millions of individuals worldwide.

The brains of sufferers of Alzheimer's disease show a characteristic pathology of prominent neuropathologic lesions, such as the initially intracellular neurofibrillary tangles (NFTs), and the extracellular amyloid-rich senile plaques. These lesions are associated with massive loss of populations of CNS neurons and their progression accompanies the clinical dementia associated with AD. The major component of amyloid plaques is the amyloid beta (A-beta) peptides of various lengths. A variant thereof, which is the A β 1-42-peptide is the major causative agent for amyloid formation. Amyloid beta is the proteolytic product of a precursor protein, beta amyloid precursor protein (beta-APP or APP). APP is a type-I trans-membrane protein which is sequentially cleaved by several different membrane-associated proteases. The first cleavage of APP occurs by one of two proteases, alpha-secretase or beta-secretase. Alpha secretase is a metalloprotease whose activity is most likely to be provided by one or a combination of the proteins ADAM10 and ADAM17. Cleavage by alpha-secretase precludes formation of amyloid peptides and is thus referred to as non-amyloidogenic. In contrast, cleavage of APP by beta-secretase is a prerequisite for subsequent formation of amyloid peptides. This secretase, also called BACE1 (beta-site APP-cleaving enzyme), is a type-I transmembrane protein containing an aspartyl protease activity (described in detail below).

The beta-secretase (BACE) activity cleaves APP in the ectodomain, resulting in shedding of secreted, soluble APP_s, and in a 99-residue C-terminal transmembrane fragment (APP-C99). Vassar et al. (Science 286, 735-741) cloned a transmembrane aspartic protease that had the characteristics of the postulated beta-secretase of APP, which they termed BACE1. Brain and primary cortical cultures from BACE1 knockout mice showed no detectable beta-secretase activity, and primary cortical cultures from BACE knockout mice produced much less amyloid-beta from APP. This suggests that BACE1, rather than its paralogue BACE2, is the main beta-secretase for APP. BACE1 is a protein of 501 amino acids containing a 21-aa signal peptide followed by a proprotein domain spanning aa 22 to 45. There are alternatively spliced forms, BACE-I-457 and BACE-I-476. The luminal domain of the mature protein is followed by one predicted transmembrane domain and a short cytosolic C-terminal tail of 24 aa. BACE1 is predicted to be a type 1 transmembrane protein with the active site on the luminal side of the membrane, where beta-secretase cleaves APP and possible other yet unidentified substrates. Although BACE1 is clearly a key enzyme required for the processing of APP into A-beta, recent evidence suggests additional potential substrates and functions of BACE1 (J. Biol. Chem. 279, 10542-10550). To date, no BACE1 interacting proteins with regulatory or modulatory functions have been described.

The APP fragment generated by BACE1 cleavage, APP-C99, is a substrate for the gamma-secretase activity, which cleaves APP-C99 within the plane of the membrane into an A-beta peptide (such as the amyloidogenic Aβ₁₋₄₂ peptide), and into a C-terminal fragment termed APP intracellular domain (AICD) (Annu Rev Cell Dev Biol 19, 25-51). The gamma-secretase activity resides within a multiprotein complex with at least four distinct subunits. The first subunit to be discovered was presenilin (Proc Natl Acad Sci USA 94, 8208-13). Other known protein components of the gamma-secretase complex are Pen-2, Nicastrin and Aph-1a

Despite recent progress in delineating molecular events underlying the etiology of Alzheimer's disease, no disease-modifying therapies have been developed so far. To this end, the industry has struggled to identify suitable lead compounds for inhibition of BACE1. Moreover, it has been recognized that a growing number of alternative substrates of gamma-secretase exist, most notably the Notch protein. Consequently, inhibition of gamma-secretase is likely to cause mechanism-based side effects. Current top drugs (e.g. Aricept®/donepezil) attempt to achieve a temporary improvement of cognitive functions by inhibiting

acetylcholinesterase, which results in increased levels of the neurotransmitter acetylcholine in the brain. These therapies are not suitable for later stages of the disease, they do not treat the underlying disease pathology, and they do not halt disease progression.

Thus, there is an unmet need for the identification of novel targets allowing novel molecular strategies for the treatment of Alzheimer's disease. In addition, there is a strong need for novel therapeutic compounds modifying the aforementioned molecular processes by targeting said novel targets.

In a first aspect, the invention provides the use of a FADS2 interacting molecule for the preparation of a pharmaceutical composition for the treatment of neurogenerative diseases.

In the context of the present invention, it has been surprisingly found that FADS2 forms part of different intracellular protein complexes which are involved in the aberrant processing of APP in Alzheimer's disease by gamma secretase. Especially, it has been found that FADS2 is part of the Nicastrin complex, of the BACE1-complex, of the Psen2-complex and of the PTK7 complex, all molecules known to interact with gamma secretase. These complexes are named after their key protein compound. Other members of these complexes are listed in table 1. However, within the meaning of the present invention it is to be understood that the definition of each of the complexes includes a complex of FADS2 and of one or more other proteins as listed in table 1, provided that these proteins belong to the same complex as indicated in table 1.

The identification of FADS2 as a key molecule in these complexes enables the use of FADS2 interacting molecules for the treatment of neurodegenerative diseases. This is especially shown in the Example-section (infra) where it is demonstrated that siRNA directed against FADS2 results in the correct processing of APP, i.e. in the formation of Abeta-40 instead of Abeta-42 by gamma secretase.

In the context of the present invention, a „FADS2 interacting molecule“ is a molecule which binds at least temporarily to FADS2 and which preferably modulates FADS2 activity.

Fatty acid $\Delta 6$ desaturase (FADS2) has been known to catalyze the rate-limiting step in the biosynthesis of polyunsaturated fatty acids (PUFA), the conversion of either linoleic acid (C18:2) into Δ -linolenic acid (gLA; C18:3n-6) in the n-6 metabolic pathway or of Δ -linolenic acid (aLA; C18:3n-3) into stearidonic acid (C18:4n-3) in the n-3 metabolic pathway. gLA is subsequently elongated and converted to arachidonic acid (AA; C20:4n-6) by fatty acid $\Delta 5$ desaturase (FADS1). AA is the essential precursor of various eicosanoids, such as prostaglandins and leukotrienes. In the n-3 metabolic pathway, FADS1 generates eicosapentaenoic acid (EPA; C20:5n-3), a PUFA that has been suggested to have neuroprotective effects (Lynch et al., 2003) and to be beneficial in the treatment of schizophrenia and depression (Emsley et al., 2003).

Another elongation step converts EPA into docosapentaenoic acid (DPA; C22:5n-3) and further to C24:5n-3. This PUFA and the analogous n-6 fatty acid, C24:4n-6, are additional substrates of FADS2, which converts them into C24:6n-3 and C24:5n-6, respectively. Both C24 PUFAs are partially oxidized in peroxisomes to give rise to docosahexaenoic acid (DHA; C22:6n-3), a major brain PUFA, and C22:5n-6, respectively.

Three human FADS family members have been cloned (see also for rodents (Cho et al (1999), J Biol Chem 274, 37335-37339; Marquardt, A (2000) Genomics 66, 175). All are fusion products composed of an N-terminal cytochrome b5-like domain and a C-terminal multiple membrane-spanning desaturase portion, both characterized by conserved His-motifs. FADS genes are clustered at 11q12-q13.1; likely arisen from gene duplication. The function of a related gene product, FADS3, is unknown, but given the high level of sequence similarity between FADS2 and FADS3 it has been proposed that FADS3 may constitute an alternative fatty acid $\Delta 6$ desaturase.

According to the present invention, the expression "FADS2" does not only mean the protein as shown in SEQ ID NO:76, but also a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions. Preferably, these low stringency conditions include hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at

40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

The same applies also to all other proteins named in the present invention. Therefore, a name of given protein or nucleic acid does not only refer to the protein or nucleic acid as depicted in the sequence listing, but also to its functionally active derivative, or to a functionally active fragment thereof, or a homologue thereof, or a variant encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, preferably under the conditions as mentioned above.

A functionally active derivative means a derivate which exerts essentially the same activity as FADS2, i.e. the conversion of either linoleic acid (C18:2) into Δ -linolenic acid (gLA; C18:3n-6) in the n-6 metabolic pathway or of Δ -linolenic acid (aLA); C18:3n-3) into stearidonic acid (C18:4n-3) in the n-3 metabolic pathway. The activity of FADS2 as well as of a functionally active derivative thereof can be measured as described in Obukowicz MG et al, The Journal of Pharmacology and Experimental Therapeutics (JPET) 287:157-166 (1998).

According to the present invention, the term "activity" as used herein, refers to the function of a molecule in its broadest sense. It generally includes, but is not limited to, biological, biochemical, physical or chemical functions of the molecule. It includes for example the enzymatic activity, the ability to interact with other molecules and ability to activate, facilitate, stabilize, inhibit, suppress or destabilize the function of other molecules, stability, ability to localize to certain subcellular locations. Where applicable, said term also relates to the function of a protein complex in its broadest sense.

According to the present invention, the terms "derivatives" or "analogs of component proteins" or "variants" as used herein preferably include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to a sequence encoding the component protein under

stringent, moderately stringent, or nonstringent conditions. It means a protein which is the outcome of a modification of the naturally occurring protein, by amino acid substitutions, deletions and additions, respectively, which derivatives still exhibit the biological function of the naturally occurring protein although not necessarily to the same degree. The biological function of such proteins can e.g. be examined by suitable available in vitro assays as provided in the invention.

The term "functionally active" as used herein refers to a polypeptide, namely a fragment or derivative, having structural, regulatory, or biochemical functions of the protein according to the embodiment of which this polypeptide, namely fragment or derivative is related to.

The term "fragment" as used herein refers to a polypeptide of at least 10, 20, 30, 40 or 50 amino acids of the component protein according to the embodiment. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids.

The term "gene" as used herein refers to a nucleic acid comprising an open reading frame encoding a polypeptide of, if not stated otherwise, the present invention, including both exon and optionally intron sequences.

The terms "homologue" or "homologous gene products" as used herein mean a protein in another species, preferably mammals, which performs the same biological function as the a protein component of the complex further described herein. Such homologues are also termed "orthologous gene products". The algorithm for the detection of orthologue gene pairs from humans and mammals or other species uses the whole genome of these organisms. First, pairwise best hits are retrieved, using a full Smith-Waterman alignment of predicted proteins. To further improve reliability, these pairs are clustered with pairwise best hits involving *Drosophila melanogaster* and *C. elegans* proteins. Such analysis is given, e.g., in Nature, 2001, 409:860-921. The homologues of the proteins according to the invention can either be isolated based on the sequence homology of the genes encoding the proteins provided herein to the genes of other species by cloning the respective gene applying conventional technology and expressing the protein from such gene, or by isolating proteins of the other species by isolating the analogous complex according to the methods provided herein or to other suitable methods commonly known in the art.

According to the functional assays provided herein, $\Delta 5$ desaturase (FADS1) does not have an effect on the metabolism of APP. Thus FADS1 (SEQ ID 122) and the orthologs thereof are excluded from the scope of the invention. Those sequences are thus excluded from the general definition of FADS2 homologs provided herein.

In contrast, FADS3 (SEQ ID 125) is explicitly included within the scope of the invention as a screening tool for compounds for the treatment of Alzheimer's disease and/or the modulation of gamma-secretase-activity

In a preferred embodiment of the present invention, the FADS2-interacting molecule is a FADS2 inhibitor.

According to the present invention the term "inhibitor" refers to a biochemical or chemical compound which preferably inhibits or reduces the activity of FADS2. This can e.g. occur via suppression of the expression of the corresponding gene. The expression of the gene can be measured by RT-PCR or Western blot analysis. Furthermore, this can occur via inhibition of the activity, e.g. by binding to FADS2.

Examples of such FADS2 inhibitors are binding proteins or binding peptides directed against FADS2, in particular against the active site of FADS2, and nucleic acids directed against the FADS2 gene

Preferably, the inhibitor is selected from the group consisting of antibodies, antisense oligonucleotides, siRNA, low molecular weight molecules (LMWs), binding peptides, aptamers, ribozymes.

LMWs are molecules which are not proteins, peptides antibodies or nucleic acids, and which exhibit a molecular weight of less than 5000 Da, preferably less than 2000 Da, more preferably less than 2000 Da, most preferably less than 500 Da. Such LMWs may be identified in High-Through-Put procedures starting from libraries. Such methods are known in the art.

The term "nucleic acids against FADS2" refers to double-stranded or single stranded DNA or RNA which, for example, inhibit the expression of the FADS2 gene or the activity of FADS2 and includes, without limitation, antisense nucleic acids, aptamers, siRNAs (small interfering RNAs) and ribozymes.

An "antisense" nucleic acid as used herein refers to a nucleic acid capable of hybridizing to a sequence-specific portion of a component protein RNA (preferably mRNA) by virtue of some sequence complementarity. The antisense nucleic acid may be complementary to a coding and/or noncoding region of a component protein mRNA. Such antisense nucleic acids that inhibit complex formation or activity have utility as therapeutics, and can be used in the treatment or prevention of disorders as described herein.

The nucleic acids, e.g. the antisense nucleic acids or siRNAs, can be synthesized chemically, e.g. in accordance with the phosphotriester method (see, for example, Uhlmann, E. & Peyman, A. (1990) *Chemical Reviews*, 90, 543-584). Aptamers are nucleic acids which bind with high affinity to a polypeptide, here FADS2. Aptamers can be isolated by selection methods such as SELEX (see e.g. Jayasena (1999) *Clin. Chem.*, 45, 1628-50; Klug and Famulok (1994) *M. Mol. Biol. Rep.*, 20, 97-107; US 5,582,981) from a large pool of different single-stranded RNA molecules. Aptamers can also be synthesized and selected in their mirror-image form, for example as the L-ribonucleotide (Nolte et al. (1996) *Nat. Biotechnol.*, 14, 1116-9; Klussmann et al. (1996) *Nat. Biotechnol.*, 14, 1112-5). Forms which have been isolated in this way enjoy the advantage that they are not degraded by naturally occurring ribonucleases and, therefore, possess greater stability.

Nucleic acids may be degraded by endonucleases or exonucleases, in particular by DNases and RNases which can be found in the cell. It is, therefore, advantageous to modify the nucleic acids in order to stabilize them against degradation, thereby ensuring that a high concentration of the nucleic acid is maintained in the cell over a long period of time (Beigelman et al. (1995) *Nucleic Acids Res.* 23:3989-94; WO 95/11910; WO 98/37240; WO 97/29116). Typically, such a stabilization can be obtained by introducing one or more internucleotide phosphorus groups or by introducing one or more non-phosphorus internucleotides.

Suitable modified internucleotides are compiled in Uhlmann and Peyman (1990), *supra* (see also Beigelman et al. (1995) *Nucleic Acids Res.* 23:3989-94; WO 95/11910; WO 98/37240; WO 97/29116). Modified internucleotide phosphate radicals and/or non-phosphorus bridges in a nucleic acid which can be employed in one of the uses according to the invention contain, for example, methyl phosphonate, phosphorothioate, phosphoramidate, phosphorodithioate and/or phosphate esters, whereas non-phosphorus internucleotide analogues contain, for example, siloxane bridges, carbonate bridges, carboxymethyl esters, acetamidate bridges and/or thioether bridges. It is also the intention that this modification should improve the durability of a pharmaceutical composition which can be employed in one of the uses according to the invention.

The use of suitable antisense nucleic acids is further described e.g. in Zheng and Kemeny (1995) *Clin. Exp. Immunol.*, 100, 380-2; Nellen and Lichtenstein (1993) *Trends Biochem. Sci.*, 18, 419-23, Stein (1992) *Leukemia*, 6, 697-74 or Yacyshyn, B. R. et al. (1998) *Gastroenterology*, 114, 1142).

Regarding antisense molecules, the following specific embodiments apply:

The present invention provides the therapeutic or prophylactic use of nucleic acids of at least six nucleotides that are antisense to a gene or cDNA encoding a component protein, or a portion thereof.

The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA, or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

In another embodiment, the present invention is directed to a method for inhibiting the expression of component protein nucleic acid sequences, in a prokaryotic or eukaryotic cell, comprising providing the cell with an effective amount of a composition comprising an antisense nucleic acid of the component protein, or a derivative thereof, of the invention.

The antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides, ranging from 6 to about 200 nucleotides. In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures, or derivatives or modified versions thereof, and either single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. USA 84:648-652; International Patent Publication No. WO 88/09810) or blood-brain barrier (see, e.g., International Patent Publication No. WO 89/10134), hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6:958-976), or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549).

In a preferred aspect of the invention, an antisense oligonucleotide is provided, preferably as single-stranded DNA. The oligonucleotide may be modified at any position in its structure with constituents generally known in the art.

The antisense oligonucleotides may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thio-uridine, 5-carboxymethylaminomethyluracil, dihydrouracil, D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, D-mannosylqueosine, 5N-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methyl-thio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

In another embodiment, the oligonucleotide comprises at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal, or an analog of the foregoing.

In yet another embodiment, the oligonucleotide is a 2'-anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641).

The oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

Throughout the invention, oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. USA 85:7448-7451), etc.

In a specific embodiment, the antisense oligonucleotides comprise catalytic RNAs, or ribozymes (see, e.g., International Patent Publication No. WO 90/11364; Sarver et al., 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue et al., 1987, FEBS Lett. 215:327-330).

In an alternative embodiment, the antisense nucleic acids of the invention are produced intracellularly by transcription from an exogenous sequence. For example, a vector can be

introduced in vivo such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the component protein. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art to be capable of replication and expression in mammalian cells. Expression of the sequences encoding the antisense RNAs can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, *Proc. Natl. Acad. Sci. USA* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, *Nature* 296:39-42), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a component protein gene, preferably a human gene. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with a component protein RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Pharmaceutical compositions of the invention (see Section "Pharmaceutical compositions and therapeutic/prophylactic administration", *infra*), comprising an effective amount of a protein component antisense nucleic acid in a pharmaceutically acceptable carrier can be administered to a patient having a disease or disorder that is of a type that expresses or overexpresses a protein complex of the present invention.

The amount of antisense nucleic acid that will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. Where possible, it is desirable to determine the antisense cytotoxicity in vitro, and then in useful animal model systems, prior to testing and use in humans.

In a specific embodiment, pharmaceutical compositions comprising antisense nucleic acids are administered via liposomes, microparticles, or microcapsules. In various embodiments of the invention, it may be useful to use such compositions to achieve sustained release of the antisense nucleic acids. In a specific embodiment, it may be desirable to utilize liposomes targeted via antibodies to specific identifiable central nervous system cell types (Leonetti et al., 1990, Proc. Natl. Acad. Sci. U.S.A. 87:2448-2451; Renneisen et al., 1990, J. Biol. Chem. 265:16337-16342).

The production and use of siRNAs as tools for RNA interference in the process to down regulate or to switch off gene expression, here FADS2 gene expression, is e.g. described in Elbashir, S. M. et al. (2001) Genes Dev., 15, 188 or Elbashir, S. M. et al. (2001) Nature, 411, 494. Preferably, siRNAs exhibit a length of less than 30 nucleotides, wherein the identity stretch of the sense strand of the siRNA is preferably at least 19 nucleotides.

Ribozymes are also suitable tools to inhibit the translation of nucleic acids, here the FADS2 gene, because they are able to specifically bind and cut the mRNAs. They are e.g. described in Amarzguioui et al. (1998) Cell. Mol. Life Sci., 54, 1175-202; Vaish et al. (1998) Nucleic Acids Res., 26, 5237-42; Persidis (1997) Nat. Biotechnol., 15, 921-2 or Couture and Stinchcomb (1996) Trends Genet., 12, 510-5.

The term "binding protein" or "binding peptide" refers to a class of proteins or peptides which bind and inhibit FADS2, without limitation, polyclonal or monoclonal antibodies, antibody fragments and protein scaffolds directed against these proteins.

According to the present invention the term antibody or antibody fragment is also understood as meaning antibodies or antigen-binding parts thereof, which have been prepared

recombinantly and, where appropriate, modified, such as chimaeric antibodies, humanized antibodies, multifunctional antibodies, bispecific or oligospecific antibodies, single-stranded antibodies and F(ab) or F(ab)₂ fragments (see, for example, EP-B1-0 368 684, US 4,816,567, US 4,816,397, WO 88/01649, WO 93/06213 or WO 98/24884), preferably produced with the help of a FAB expression library.

As an alternative to the classical antibodies it is also possible, for example, to use protein scaffolds against FADS2, e.g. anticalins which are based on lipocalin (Beste et al. (1999) Proc. Natl. Acad. Sci. USA, 96, 1898-1903). The natural ligand-binding sites of the lipocalins, for example the retinol-binding protein or the bilin-binding protein, can be altered, for example by means of a "combinatorial protein design" approach, in such a way that they bind to selected haptens, here to FADS2 (Skerra, 2000, Biochim. Biophys. Acta, 1482, 337-50). Other known protein scaffolds are known as being alternatives to antibodies for molecular recognition (Skerra (2000) J. Mol. Recognit., 13, 167-187).

The procedure for preparing an antibody or antibody fragment is effected in accordance with methods which are well known to the skilled person, e.g. by immunizing a mammal, for example a rabbit, with FADS2, where appropriate in the presence of, for example, Freund's adjuvant and/or aluminium hydroxide gels (see, for example, Diamond, B.A. et al. (1981) The New England Journal of Medicine: 1344-1349). The polyclonal antibodies which are formed in the animal as a result of an immunological reaction can subsequently be isolated from the blood using well known methods and, for example, purified by means of column chromatography. Monoclonal antibodies can, for example, be prepared in accordance with the known method of Winter & Milstein (Winter, G. & Milstein, C. (1991) Nature, 349, 293-299).

In detail, polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide as an immunogen. Preferred polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred polyclonal antibody preparations are ones that contain only antibodies directed against a given polypeptide or polypeptides. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a polypeptide of the invention. In such a manner, the only human epitope or

epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules can be isolated from the mammal (e.g., from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected for (e.g., partially purified) or purified by, e.g., affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those on the desired protein or polypeptide of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, e.g., when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, 1975, *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor et al., 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* 1994, Coligan et al. (eds.) John Wiley & Sons, Inc., New York, NY). Hybridoma cells producing a monoclonal antibody of the invention are detected by

screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, e.g., using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al., 1991, *Bio/Technology* 9:1370-1372; Hay et al., 1992, *Hum. Antibod. Hybridomas* 3:81-85; Huse et al., 1989, *Science* 246:1275-1281; Griffiths et al., 1993, *EMBO J.* 12:725-734.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567;

European Patent Application 125,023; Better et al., 1988, *Science* 240:1041-1043; Liu et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu et al., 1987, *J. Immunol.* 139:3521-3526; Sun et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura et al., 1987, *Canc. Res.* 47:999-1005; Wood et al., 1985, *Nature* 314:446-449; and Shaw et al., 1988, *J. Natl. Cancer Inst.* 80:1553-1559; Morrison, 1985, *Science* 229:1202-1207; Oi et al., 1986, *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones et al., 1986, *Nature* 321:552-525; Verhoeyan et al., 1988, *Science* 239:1534; and Beidler et al., 1988, *J. Immunol.* 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, 1995, *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., 1994, *Bio/technology* 12:899-903).

Antibody fragments that contain the idiotypes of the complex can be generated by techniques known in the art. For example, such fragments include, but are not limited to, the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragment that can be generated by reducing the disulfide bridges of the F(ab')₂ fragment; the Fab fragment that can be generated by treating the antibody molecular with papain and a reducing agent; and Fv fragments.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g., ELISA (enzyme-linked immunosorbent assay). To select antibodies specific to a particular domain of the complex, or a derivative thereof, one may assay generated hybridomas for a product that binds to the fragment of the complex, or a derivative thereof, that contains such a domain. For selection of an antibody that specifically binds a complex of the present, or a derivative, or homologue thereof, but which does not specifically bind to the individual proteins of the complex, or a derivative, or homologue thereof, one can select on the basis of positive binding to the complex and a lack of binding to the individual protein components.

The foregoing antibodies can be used in methods known in the art relating to the localization and/or quantification of the given protein or proteins, e.g., for imaging these proteins, measuring levels thereof in appropriate physiological samples (by immunoassay), in diagnostic methods, etc. This hold true also for a derivative, or homologue thereof of a complex.

In a preferred embodiment, the FADS2 inhibitor is either a siRNA with the sequences: GCUGAAAUACCUGCCCUAC or GCAUGGCAUUGAAUACCAG or the compound SC-26196 (see Obukowicz, *supra*).

As discussed above, FADS2 is part of protein complexes which are involved in the regulation of gamma secretase activity and/or beta-secretase. Therefore, in a preferred embodiment, the FADS2 interacting molecule or inhibitor acts on a FADS2 molecule which is part of a protein complex comprising at least on further protein selected from the proteins in table 1, third column. Preferably, FADS2 is part of one of the compexes that are shown in Table 1, wherein

in this context "complex" means that apart from FADS2 at least one of the proteins of one of the complexes is present. These complexes include the three Nicastrin complexes (a), (b) and (c), the BACE1-complex (a) and (b), the Psen2-complex as well as the PTK7 complex.

Said protein complexes have been identified as assemblies of proteins interacting with the gamma-secretase components Nicastrin and Psen-2 and with beta-secretase protein BACE1 as well as with PTK7, itself a member of the BACE1 complex.

Presenilins 1 and 2 (Psen1 and Psen2, also referred to as PS1 and PS2 respectively) are integral membrane proteins which are localised in the endoplasmic reticulum, the Golgi and also at the cell surface (Kovacs, *Nat Med* 2, 224). They are predominantly found as a heterodimers of the NTF and CTF endoproteolytic fragments. The protease that cleaves presenilins (the "presenilinase") is not known, it is likely that the process is autocatalytic, also the functional significance of PS (auto)proteolysis is unclear. Presenilins are involved in the proteolytical processing of Amyloid precursor protein (APP) (De Strooper et al, *Nature* 391, 387) and the Notch receptor (De Strooper et al, *Nature* 398, 518). In addition, Presenilins are associated with the cell-adhesion proteins alpha and beta-catenin, N-cadherin, and E-cadherin (Georgakopoulos et al, *Mol Cell* 4, 893) and other members of the armadillo family (Yu et al, *J Biol Chem* 273, 16470). APP processing by Presenilins is through their effects on gamma-secretase which cleaves APP, generating the C-terminus of the A-beta peptide. PS1 associates with the C83 and C99 processed C-terminal fragments of APP (Xia et al, *Proc Natl Acad Sci USA*, 94, 8208), Nicastrin (Yu et al, *Nature* 407, 48) and Pen-2 (Francis et al, *Dev Cell* 3, 85). Aph-1 (Francis et al, *Dev Cell* 3, 85) is required in Presenilin processing. It is not clear whether Presenilins regulate gamma-secretase activity directly or whether they are protease enzymes themselves (Kopan and Gouate, *Genes Dev* 14, 2799). The gamma secretase activity could comprise a multimeric complex of these proteins (Yu et al, *Nature* 407, 48) but it is not known how the relationship between these proteins affects secretase activity.

Nicastrin is a type 1 trans-membrane glycoprotein with a conserved transmembrane domain and DYIGS motif (Yu et al, *Nature* 407, 48) which is constitutively expressed in neural cell lines (Sato and Kuroda, *Neuropathology* 21, 115). Biochemical studies have shown that Nicastrin binds to Presenilins 1 and 2, C-terminal derivatives of APP (Yu et al, *Nature* 407, 48), membrane-tethered forms of Notch (Chen et al, *Nat Cell Biol* 3, 751) and that it is a

member of the gamma-secretase complex along with PS1 and PS2. It has been shown that Nicastrin is required for the intra-membrane cleavage of Notch (Lopez-Schier and St Johnston, *Dev Cell* 2, 79) and APP (Chung and Struhl, *Nat Cell Biol* 3, 1129), it may also have a role in post-translational stabilisation of Presenilin (Hu et al, *Dev Cell* 2, 69).

Protein Tyrosine Kinase 7 (PTK7), also referred to as colon carcinoma kinase 4 (CCK4), is an immunoglobulin superfamily transmembrane glycoprotein related to chicken KLG and *D. melanogaster* off-track. The gene has been mapped to human chromosome 6p21.1-->p12.2 by fluorescence in situ hybridization (Banga et al., 1997, *Cytogenet Cell Genet.* 1997;76(1-2):43-4). PTK7, several splicing variants of which exist in human tissues, differs from the receptor tyrosine kinase consensus sequence in several positions, suggesting that the protein be catalytically inactive (Mossie et al., 1995, *Oncogene.* 1995 Nov 16;11(10):2179-84.). PTK7 is expressed in multiple human tissues, but its function is unknown. However, its similarity to the *D. melanogaster* transmembrane protein Off-track/Dtrk, which serves as a coreceptor of plexin A for semaphorins Sema 1A (Winberg et al., *Neuron.* 2001 Oct 11;32(1):53-62) and Sema 6D (Toyofuku et al., *Genes Dev.* 2004 Feb 15;18(4):435-47.), suggests that PTK7 might act as a coreceptor of a plexin-like protein. In the CNS, PTK7 might therefore play a role in maintenance of neuronal connectivity.

The beta-secretase (BACE) activity cleaves APP in the ectodomain, resulting in shedding of secreted, soluble APP_b, and in a 99-residue C-terminal transmembrane fragment (APP-C99). Vassar et al. (*Science* 286, 735-741) cloned a transmembrane aspartic protease that had the characteristics of the postulated beta-secretase of APP, which they termed BACE1. Brain and primary cortical cultures from BACE1 knockout mice showed no detectable beta-secretase activity, and primary cortical cultures from BACE knockout mice produced much less amyloid-beta from APP. This suggests that BACE1, rather than its paralogue BACE2, is the main beta-secretase for APP. BACE1 is a protein of 501 amino acids containing a 21-aa signal peptide followed by a proprotein domain spanning aa 22 to 45. There are alternatively spliced forms, BACE-I-457 and BACE-I-476. The luminal domain of the mature protein is followed by one predicted transmembrane domain and a short cytosolic C-terminal tail of 24 aa. BACE1 is predicted to be a type 1 transmembrane protein with the active site on the luminal side of the membrane, where beta-secretase cleaves APP and possible other yet unidentified substrates. Although BACE1 is clearly a key enzyme required for the processing

of APP into A-beta, recent evidence suggests additional potential substrates and functions of BACE1 (J. Biol. Chem. 279, 10542-10550). To date, no BACE1 interacting proteins with regulatory or modulatory functions have been described.

The elucidation of these protein interactors provides novel intervention points for therapy.

As explained above, it has been surprisingly found in the context of the present invention that FADS2 is part of the protein complexes regulating beta-secretase and/or gamma secretase activity. Therefore, in a preferred embodiment, the inhibitor or interacting molecule modulates the activity of beta- secretase and/or gamma secretase.

In the context of the present invention, "modulating the activity of gamma secretase and/or beta secretase" means that the activity is reduced in that less or no product is formed (partial or complete inhibition) or that the respective enzyme produces a different product (in the case of gamma secretase e.g. Abeta-40 instead of Abeta-42) or that the relative quantities of the products are different (in the case of gamma secretase e.g. more Abeta-40 than Abeta-42). Furthermore, it is included that the modulator modulates either gamma secretase or beta secretase or the activity of both enzymes.

Throughout the invention, it is preferred that the beta secretase modulator inhibits the activity of beta secretase either completely or partially.

With respect to the modulator of gamma secretase activity, it is preferred that this modulator inhibits gamma secretase activity. However, it is also preferred that the activity of gamma secretase is shifted in a way that more Abeta-40 is produced instead of Abeta-42.

Gamma secretase activity can e.g. measured by determining APP processing, e.g. by determining whether Abeta-40 or Abeta-42 is produced (see Example-section, infra).

To measure BACE1 activity, changes of the ratio between alpha- and beta-C-terminal APP fragments can be analyzed by Western Blotting (Blasko et al., J Neural Transm 111, 523); additional examples for BACE1 activity assays include but are not limited to: use of a cyclized enzyme donor peptide containing a BACE1 cleavage site to reconstitute and measure

beta-galactosidase reporter activity (Naqvi et al., J Biomol Screen. 9, 398); use of quenched fluorimetric peptide substrates and fluorescence measurements (Andrau et al., J.Biol Chem 278, 25859); use of cell-based assays utilizing recombinant chimeric proteins, in which an enzyme (such as alkaline phosphatase) is linked via a stretch of amino acids, that contain the BACE1 recognition sequence, to a Golgi-resident protein (Oh et al., Anal Biochem, 323, 7); fluorescence resonance energy transfer (FRET)-based assays (Kennedy et al., Anal Biochem 319, 49); a cellular growth selection system in yeast (Luthi et al., Biochim Biophys Acta 1620, 167).

Preferably, the neurodegenerative disease is Alzheimer's disease.

According to the invention, the FADS2 interacting molecule is used to prepare a pharmaceutical composition.

The invention provides pharmaceutical compositions, which may be administered to a subject in an effective amount. In a preferred aspect, the therapeutic is substantially purified. The subject is preferably an animal including, but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human. In a specific embodiment, a non-human mammal is the subject.

Various delivery systems are known and can be used to administer a therapeutic of the invention, e.g., encapsulation in liposomes, microparticles, and microcapsules; use of recombinant cells capable of expressing the therapeutic, use of receptor-mediated endocytosis (e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432); construction of a therapeutic nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds may be administered by any convenient route, for example by infusion, by bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral, rectal and intestinal mucosa, etc.), and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example,

attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment. This may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

In another embodiment, the therapeutic can be delivered in a vesicle, in particular a liposome (Langer, 1990, *Science* 249:1527-1533; Treat et al., 1989, In: *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler, eds., Liss, New York, pp. 353-365; Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the therapeutic can be delivered via a controlled release system. In one embodiment, a pump may be used (Langer, *supra*; Sefton, 1987, *CRC Crit. Rev. Biomed. Eng.* 14:201-240; Buchwald et al., 1980, *Surgery* 88:507-516; Saudek et al., 1989, *N. Engl. J. Med.* 321:574-579). In another embodiment, polymeric materials can be used (*Medical Applications of Controlled Release*, Langer and Wise, eds., CRC Press, Boca Raton, Florida, 1974; *Controlled Drug Bioavailability, Drug Product Design and Performance*, Smolen and Ball, eds., Wiley, New York, 1984; Ranger and Peppas, 1983, *Macromol. Sci. Rev. Macromol. Chem.* 23:61; Levy et al., 1985, *Science* 228:190-192; During et al., 1989, *Ann. Neurol.* 25:351-356; Howard et al., 1989, *J. Neurosurg.* 71:858-863). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (e.g., Goodson, 1984, In: *Medical Applications of Controlled Release*, *supra*, Vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer (1990, *Science* 249:1527-1533).

In a specific embodiment where the therapeutic is a nucleic acid encoding a protein therapeutic, the nucleic acid can be administered *in vivo* to promote expression of its encoded

protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or by coating it with lipids, cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (e.g., Joliot et al., 1991, Proc. Natl. Acad. Sci. USA 88:1864-1868), etc. Alternatively, a nucleic acid therapeutic can be introduced intracellularly and incorporated by homologous recombination within host cell DNA for expression.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a therapeutic, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly, in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, including but not limited to peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered orally. Saline and aqueous dextrose are preferred carriers when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are preferably employed as liquid carriers for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsions, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the

therapeutic, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated, in accordance with routine procedures, as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water or saline for injection can be provided so that the ingredients may be mixed prior to administration.

The therapeutics of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free carboxyl groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., those formed with free amine groups such as those derived from isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc., and those derived from sodium, potassium, ammonium, calcium, and ferric hydroxides, etc.

The amount of the therapeutic of the invention which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. However, suitable dosage ranges for intravenous administration are generally about 20-500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1

mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The kits of the present invention can also contain expression vectors encoding the essential components of the complex machinery, which components after being expressed can be reconstituted in order to form a biologically active complex. Such a kit preferably also contains the required buffers and reagents. Optionally associated with such container(s) can be instructions for use of the kit and/or a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The invention further relates to a method of treatment, wherein an effective amount of a FADS2 interacting molecule or inhibitor is administered to a subject suffering from a neurodegenerative disease, preferably Alzheimer's disease.

With respect to this method of the invention, all embodiments apply given above for the use of the invention.

The invention further relates to a method for identifying a gamma secretase modulator and/or beta-secretase modulator, comprising the following steps:

- a. identifying of a FADS2-interacting molecule by determining whether a given test compound is a FADS2-interacting molecule,
- b. determining whether the FADS2-interacting molecule of step a) is capable of modulating gamma secretase activity or beta-secretase activity.

In a preferred embodiment of the invention, in step a) the test compound is brought into contact with FADS2 and the interaction of FADS2 with the test compound is determined. Preferably, it is measured whether the candidate molecule is bound to FADS2.

The method of the invention is preferably performed in the context of a high throughput assay. Such assays are known to the person skilled in the art.

Test or candidate molecules to be screened can be provided as mixtures of a limited number of specified compounds, or as compound libraries, peptide libraries and the like. Agents/molecules to be screened may also include all forms of antisera, antisense nucleic acids, etc., that can modulate complex activity or formation. Exemplary candidate molecules and libraries for screening are set forth below.

Screening the libraries can be accomplished by any of a variety of commonly known methods. See, e.g., the following references, which disclose screening of peptide libraries: Parmley and Smith, 1989, *Adv. Exp. Med. Biol.* 251:215-218; Scott and Smith, 1990, *Science* 249:386-390; Fowlkes et al., 1992, *BioTechniques* 13:422-427; Oldenburg et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:5393-5397; Yu et al., 1994, *Cell* 76:933-945; Staudt et al., 1988, *Science* 241:577-580; Bock et al., 1992, *Nature* 355:564-566; Tuerk et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:6988-6992; Ellington et al., 1992, *Nature* 355:850-852; U.S. Patent No. 5,096,815, U.S. Patent No. 5,223,409, and U.S. Patent No. 5,198,346, all to Ladner et al.; Rebar and Pabo, 1993, *Science* 263:671-673; and International Patent Publication No. WO 94/18318.

In a specific embodiment, screening can be carried out by contacting the library members with a FADS2 immobilized on a solid phase, and harvesting those library members that bind to the protein (or encoding nucleic acid or derivative). Examples of such screening methods,

termed "panning" techniques, are described by way of example in Parmley and Smith, 1988, Gene 73:305-318; Fowlkes et al., 1992, BioTechniques 13:422-427; International Patent Publication No. WO 94/18318; and in references cited hereinabove.

In a specific embodiment, FADS 2 fragments and/or analogs, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of the formation of a complex of FADS2 with another proteins, e.g. the proteins given in Table 1 (amount of complex or composition of complex) or FADS2 activity in the cell, which thereby inhibit complex activity or formation in the cell.

In one embodiment, agents that modulate (i.e., antagonize or agonize) FADS2 activity or FADS2-protein complex formation can be screened for using a binding inhibition assay, wherein agents are screened for their ability to modulate formation of a complex under aqueous, or physiological, binding conditions in which complex formation occurs in the absence of the agent to be tested. Agents that interfere with the formation of complexes of the invention are identified as antagonists of complex formation. Agents that promote the formation of complexes are identified as agonists of complex formation. Agents that completely block the formation of complexes are identified as inhibitors of complex formation.

Methods for screening may involve labeling the component proteins of the complex with radioligands (e.g., ^{125}I or ^3H), magnetic ligands (e.g., paramagnetic beads covalently attached to photobiotin acetate), fluorescent ligands (e.g., fluorescein or rhodamine), or enzyme ligands (e.g., luciferase or β -galactosidase). The reactants that bind in solution can then be isolated by one of many techniques known in the art, including but not restricted to, co-immunoprecipitation of the labeled complex moiety using antisera against the unlabeled binding partner (or labeled binding partner with a distinguishable marker from that used on the second labeled complex moiety), immunoaffinity chromatography, size exclusion chromatography, and gradient density centrifugation. In a preferred embodiment, the labeled binding partner is a small fragment or peptidomimetic that is not retained by a commercially available filter. Upon binding, the labeled species is then unable to pass through the filter, providing for a simple assay of complex formation.

Methods commonly known in the art are used to label at least one of the component members of the complex. Suitable labeling methods include, but are not limited to, radiolabeling by incorporation of radiolabeled amino acids, e.g., ^3H -leucine or ^{35}S -methionine, radiolabeling by post-translational iodination with ^{125}I or ^{131}I using the chloramine T method, Bolton-Hunter reagents, etc., or labeling with ^{32}P using phosphorylase and inorganic radiolabeled phosphorous, biotin labeling with photobiotin-acetate and sunlamp exposure, etc. In cases where one of the members of the complex is immobilized, e.g., as described infra, the free species is labeled. Where neither of the interacting species is immobilized, each can be labeled with a distinguishable marker such that isolation of both moieties can be followed to provide for more accurate quantification, and to distinguish the formation of homomeric from heteromeric complexes. Methods that utilize accessory proteins that bind to one of the modified interactants to improve the sensitivity of detection, increase the stability of the complex, etc., are provided.

Typical binding conditions are, for example, but not by way of limitation, in an aqueous salt solution of 10-250 mM NaCl, 5-50 mM Tris-HCl, pH 5-8, and 0.5% Triton X-100 or other detergent that improves specificity of interaction. Metal chelators and/or divalent cations may be added to improve binding and/or reduce proteolysis. Reaction temperatures may include 4, 10, 15, 22, 25, 35, or 42 degrees Celsius, and time of incubation is typically at least 15 seconds, but longer times are preferred to allow binding equilibrium to occur. Particular complexes can be assayed using routine protein binding assays to determine optimal binding conditions for reproducible binding.

The physical parameters of complex formation can be analyzed by quantification of complex formation using assay methods specific for the label used, e.g., liquid scintillation counting for radioactivity detection, enzyme activity for enzyme-labeled moieties, etc. The reaction results are then analyzed utilizing Scatchard analysis, Hill analysis, and other methods commonly known in the arts (see, e.g., *Proteins, Structures, and Molecular Principles*, 2nd Edition (1993) Creighton, Ed., W.H. Freeman and Company, New York).

In a second common approach to binding assays, one of the binding species is immobilized on a filter, in a microtiter plate well, in a test tube, to a chromatography matrix, etc., either covalently or non-covalently. Proteins can be covalently immobilized using any method well

known in the art, for example, but not limited to the method of Kadonaga and Tjian, 1986, Proc. Natl. Acad. Sci. USA 83:5889-5893, i.e., linkage to a cyanogen-bromide derivatized substrate such as CNBr-Sepharose 4B (Pharmacia). Where needed, the use of spacers can reduce steric hindrance by the substrate. Non-covalent attachment of proteins to a substrate include, but are not limited to, attachment of a protein to a charged surface, binding with specific antibodies, binding to a third unrelated interacting protein, etc.

Assays of agents (including cell extracts or a library pool) for competition for binding of one member of a complex (or derivatives thereof) with another member of the complex labeled by any means (e.g., those means described above) are provided to screen for competitors or enhancers of complex formation.

In specific embodiments, blocking agents to inhibit non-specific binding of reagents to other protein components, or absorptive losses of reagents to plastics, immobilization matrices, etc., are included in the assay mixture. Blocking agents include, but are not restricted to bovine serum albumin, casein, nonfat dried milk, Denhardt's reagent, Ficoll, polyvinylpyrrolidone, nonionic detergents (NP40, Triton X-100, Tween 20, Tween 80, etc.), ionic detergents (e.g., SDS, LDS, etc.), polyethylene glycol, etc. Appropriate blocking agent concentrations allow complex formation.

After binding is performed, unbound, labeled protein is removed in the supernatant, and the immobilized protein retaining any bound, labeled protein is washed extensively. The amount of bound label is then quantified using standard methods in the art to detect the label as described, supra.

In another specific embodiments screening for modulators of the protein complexes/protein as provided herein can be carried out by attaching those and/or the antibodies as provided herein to a solid carrier.

The preparation of such an array containing different types of proteins, including antibodies) is well known in the art and is apparent to a person skilled in the art (see e.g. Ekins et al., 1989, J. Pharm. Biomed. Anal. 7:155-168; Mitchell et al. 2002, Nature Biotechnol. 20:225-229; Petricoin et al., 2002, Lancet 359:572-577; Templin et al., 2001, Trends Biotechnol.

20:160-166; Wilson and Nock, 2001, *Curr. Opin. Chem. Biol.* 6:81-85; Lee et al., 2002 *Science* 295:1702-1705; MacBeath and Schreiber, 2000, *Science* 289:1760; Blawas and Reichert, 1998, *Biomaterials* 19:595; Kane et al., 1999, *Biomaterials* 20:2363; Chen et al., 1997, *Science* 276:1425; Vaughan et al., 1996, *Nature Biotechnol.* 14:309-314; Mahler et al., 1997, *Immunotechnology* 3:31-43; Roberts et al., 1999, *Curr. Opin. Chem. Biol.* 3:268-273; Nord et al., 1997, *Nature Biotechnol.* 15:772-777; Nord et al., 2001, *Eur. J. Biochem.* 268:4269-4277; Brody and Gold, 2000, *Rev. Mol. Biotechnol.* 74:5-13; Karlstroem and Nygren, 2001, *Anal. Biochem.* 295:22-30; Nelson et al., 2000, *Electrophoresis* 21:1155-1163; Honore et al., 2001, *Expert Rev. Mol. Diagn.* 3:265-274; Albala, 2001, *Expert Rev. Mol. Diagn.* 2:145-152, Figeys and Pinto, 2001, *Electrophoresis* 2:208-216 and references in the publications listed here).

Complexes can be attached to an array by different means as will be apparent to a person skilled in the art. Complexes can for example be added to the array via a TAP-tag (as described in WO/0009716 and in Rigaut et al., 1999, *Nature Biotechnol.* 10:1030-1032) after the purification step or by another suitable purification scheme as will be apparent to a person skilled in the art.

Optionally, the proteins of the complex can be cross-linked to enhance the stability of the complex. Different methods to cross-link proteins are well known in the art. Reactive end-groups of cross-linking agents include but are not limited to -COOH, -SH, -NH₂ or N-oxy-succinamate.

The spacer of the cross-linking agent should be chosen with respect to the size of the complex to be cross-linked. For small protein complexes, comprising only a few proteins, relatively short spacers are preferable in order to reduce the likelihood of cross-linking separate complexes in the reaction mixture. For larger protein complexes, additional use of larger spacers is preferable in order to facilitate cross-linking between proteins within the complex.

It is preferable to check the success-rate of cross-linking before linking the complex to the carrier.

As will be apparent to a person skilled in the art, the optimal rate of cross-linking need to be determined on a case by case basis. This can be achieved by methods well known in the art, some of which are exemplary described below.

A sufficient rate of cross-linking can be checked f.e. by analysing the cross-linked complex vs. a non-cross-linked complex on a denaturing protein gel.

If cross-linking has been performed successfully, the proteins of the complex are expected to be found in the same lane, whereas the proteins of the non-cross-linked complex are expected to be separated according to their individual characteristics. Optionally the presence of all proteins of the complex can be further checked by peptide-sequencing of proteins in the respective bands using methods well known in the art such as mass spectrometry and/or Edman degradation.

In addition, a rate of crosslinking which is too high should also be avoided. If cross-linking has been carried out too extensively, there will be an increasing amount of cross-linking of the individual protein complex, which potentially interferes with a screening for potential binding partners and/or modulators etc. using the arrays.

The presence of such structures can be determined by methods well known in the art and include e.g. gel-filtration experiments comparing the gel filtration profile solutions containing cross-linked complexes vs. uncross-linked complexes.

Optionally, functional assays as will be apparent to a person skilled in the art, some of which are exemplarily provided herein, can be performed to check the integrity of the complex.

Alternatively, the proteins or the protein can be expressed as a single fusion protein and coupled to the matrix as will be apparent to a person skilled in the art.

Optionally, the attachment of the complex or proteins or antibody as outlined above can be further monitored by various methods apparent to a person skilled in the art. Those include, but are not limited to surface plasmon resonance (see e.g. McDonnel, 2001, Curr. Opin. Chem. Biol. 5:572-577; Lee, 2001, Trends Biotechnol. 19:217-222; Weinberger et al., 2000,

1:395-416; Pearson et al., 2000, *Ann. Clin. Biochem.* 37:119-145; Vely et al., 2000, *Methods Mol. Biol.* 121:313-321; Slepak, 2000, *J. Mol. Recognit.* 13:20-26.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA include but are not limited to those described in Vassar R et al., 1999, *Science*, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot include but are not limited to those described in Yan R et al., 1999, *Nature*, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, BACE1-complex, PTK7-complex include but are not limited to those described in Tian G et al., 2002; *J Biol Chem*, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, PTK7-complex, BACE1-complex, include but are not limited to those described in Cao X et al., 2001, *Science*, 293:115-20.

Any molecule known in the art can be tested for its ability to be an interacting molecule or inhibitor according to the present invention. Candidate molecules can be directly provided to a cell expressing the FADS2-complex machinery, or, in the case of candidate proteins, can be provided by providing their encoding nucleic acids under conditions in which the nucleic acids are recombinantly expressed to produce the candidate protein.

The method of the invention is well suited to screen chemical libraries for molecules which modulate, e.g., inhibit, antagonize, or agonize, the amount of, activity of, or protein component composition of the complex. The chemical libraries can be peptide libraries,

peptidomimetic libraries, chemically synthesized libraries, recombinant, e.g., phage display libraries, and in vitro translation-based libraries, other non-peptide synthetic organic libraries, etc.

Exemplary libraries are commercially available from several sources (ArQule, Tripos/PanLabs, ChemDesign, Pharmacopoeia). In some cases, these chemical libraries are generated using combinatorial strategies that encode the identity of each member of the library on a substrate to which the member compound is attached, thus allowing direct and immediate identification of a molecule that is an effective modulator. Thus, in many combinatorial approaches, the position on a plate of a compound specifies that compound's composition. Also, in one example, a single plate position may have from 1-20 chemicals that can be screened by administration to a well containing the interactions of interest. Thus, if modulation is detected, smaller and smaller pools of interacting pairs can be assayed for the modulation activity. By such methods, many candidate molecules can be screened.

Many diversity libraries suitable for use are known in the art and can be used to provide compounds to be tested according to the present invention. Alternatively, libraries can be constructed using standard methods. Chemical (synthetic) libraries, recombinant expression libraries, or polysome-based libraries are exemplary types of libraries that can be used.

The libraries can be constrained or semirigid (having some degree of structural rigidity), or linear or unconstrained. The library can be a cDNA or genomic expression library, random peptide expression library or a chemically synthesized random peptide library, or non-peptide library. Expression libraries are introduced into the cells in which the assay occurs, where the nucleic acids of the library are expressed to produce their encoded proteins.

In one embodiment, peptide libraries that can be used in the present invention may be libraries that are chemically synthesized in vitro. Examples of such libraries are given in Houghten et al., 1991, *Nature* 354:84-86, which describes mixtures of free hexapeptides in which the first and second residues in each peptide were individually and specifically defined; Lam et al., 1991, *Nature* 354:82-84, which describes a "one bead, one peptide" approach in which a solid phase split synthesis scheme produced a library of peptides in which each bead in the collection had immobilized thereon a single, random sequence of amino acid residues;

Medynski, 1994, *Bio/Technology* 12:709-710, which describes split synthesis and T-bag synthesis methods; and Gallop et al., 1994, *J. Med. Chem.* 37:1233-1251. Simply by way of other examples, a combinatorial library may be prepared for use, according to the methods of Ohlmeyer et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:10922-10926; Erb et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:11422-11426; Houghten et al., 1992, *Biotechniques* 13:412; Jayawickreme et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:1614-1618; or Salmon et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:11708-11712. PCT Publication No. WO 93/20242 and Brenner and Lerner, 1992, *Proc. Natl. Acad. Sci. USA* 89:5381-5383 describe "encoded combinatorial chemical libraries," that contain oligonucleotide identifiers for each chemical polymer library member.

In a preferred embodiment, the library screened is a biological expression library that is a random peptide phage display library, where the random peptides are constrained (e.g., by virtue of having disulfide bonding).

Further, more general, structurally constrained, organic diversity (e.g., nonpeptide) libraries, can also be used. By way of example, a benzodiazepine library (see e.g., Bunin et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:4708-4712) may be used.

Conformationally constrained libraries that can be used include but are not limited to those containing invariant cysteine residues which, in an oxidizing environment, cross-link by disulfide bonds to form cystines, modified peptides (e.g., incorporating fluorine, metals, isotopic labels, are phosphorylated, etc.), peptides containing one or more non-naturally occurring amino acids, non-peptide structures, and peptides containing a significant fraction of γ -carboxyglutamic acid.

Libraries of non-peptides, e.g., peptide derivatives (for example, that contain one or more non-naturally occurring amino acids) can also be used. One example of these are peptoid libraries (Simon et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:9367-9371). Peptoids are polymers of non-natural amino acids that have naturally occurring side chains attached not to the α carbon but to the backbone amino nitrogen. Since peptoids are not easily degraded by human digestive enzymes, they are advantageously more easily adaptable to drug use. Another example of a library that can be used, in which the amide functionalities in peptides

have been permethylated to generate a chemically transformed combinatorial library, is described by Ostresh et al., 1994, Proc. Natl. Acad. Sci. USA 91:11138-11142).

The members of the peptide libraries that can be screened according to the invention are not limited to containing the 20 naturally occurring amino acids. In particular, chemically synthesized libraries and polysome based libraries allow the use of amino acids in addition to the 20 naturally occurring amino acids (by their inclusion in the precursor pool of amino acids used in library production). In specific embodiments, the library members contain one or more non-natural or non-classical amino acids or cyclic peptides. Non-classical amino acids include but are not limited to the D-isomers of the common amino acids, α -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid; γ -Abu, γ -Ahx, 6-amino hexanoic acid; Aib, 2-amino isobutyric acid; 3-amino propionic acid; ornithine; norleucine; norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, designer amino acids such as β -methyl amino acids, C-methyl amino acids, N-methyl amino acids, fluoro-amino acids and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

In a specific embodiment, fragments and/or analogs of complexes of the invention, or protein components thereof, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex activity or formation.

In another embodiment of the present invention, combinatorial chemistry can be used to identify modulators of a the complexes. Combinatorial chemistry is capable of creating libraries containing hundreds of thousands of compounds, many of which may be structurally similar. While high throughput screening programs are capable of screening these vast libraries for affinity for known targets, new approaches have been developed that achieve libraries of smaller dimension but which provide maximum chemical diversity. (See e.g., Matter, 1997, J. Med. Chem. 40:1219-1229).

One method of combinatorial chemistry, affinity fingerprinting, has previously been used to test a discrete library of small molecules for binding affinities for a defined panel of proteins. The fingerprints obtained by the screen are used to predict the affinity of the individual library members for other proteins or receptors of interest (in the instant invention, the protein

complexes of the present invention and protein components thereof.) The fingerprints are compared with fingerprints obtained from other compounds known to react with the protein of interest to predict whether the library compound might similarly react. For example, rather than testing every ligand in a large library for interaction with a complex or protein component, only those ligands having a fingerprint similar to other compounds known to have that activity could be tested. (See, e.g., Kauvar et al., 1995, *Chem. Biol.* 2:107-118; Kauvar, 1995, *Affinity fingerprinting*, Pharmaceutical Manufacturing International. 8:25-28; and Kauvar, *Toxic-Chemical Detection by Pattern Recognition in New Frontiers in Agrochemical Immunoassay*, Kurtz, Stanker and Skerritt (eds), 1995, AOAC: Washington, D.C., 305-312).

Kay et al. (1993, *Gene* 128:59-65) disclosed a method of constructing peptide libraries that encode peptides of totally random sequence that are longer than those of any prior conventional libraries. The libraries disclosed in Kay et al. encode totally synthetic random peptides of greater than about 20 amino acids in length. Such libraries can be advantageously screened to identify complex modulators. (See also U.S. Patent No. 5,498,538 dated March 12, 1996; and PCT Publication No. WO 94/18318 dated August 18, 1994).

A comprehensive review of various types of peptide libraries can be found in Gallop et al., 1994, *J. Med. Chem.* 37:1233-1251.

In a preferred embodiment, the interaction of the test compound with FADS2 results in an inhibition of FADS2 activity.

According to a preferred embodiment, in step b) the ability of the gamma secretase to cleave APP is measured. This can be measured as indicated above.

Further, the invention also relates to a method for preparing a pharmaceutical composition for the treatment of neurodegenerative diseases, comprising the following steps:

- a) identifying a gamma secretase modulator and/or beta-secretase modulator according to the method of the invention, and
- b) formulating the gamma secretase modulator to a pharmaceutical composition.

With respect to the pharmaceutical composition, all embodiments as indicated above apply also here.

The invention further relates to protein complexes comprising FADS2 and at least a further protein. As indicated above, in the context of the present invention, these protein complexes have been identified for the first time.

Therefore, in a further aspect, the invention relates to a protein complex comprising

- a) FADS2 and
- b) either one or more proteins of the Nicastrin (a) complex, of the Nicastrin (b) complex, of the Nicastrin (c) complex, of the BACE1-complex (a), of the BACE1-complex (b), of the Psen2-complex or of the PTK7 complex.

In a preferred embodiment, the one or more proteins of the Nicastrin (a) complex are selected from the group consisting of

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53)
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119)
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103),
- (iv) "Aph-1a" (SEQ ID No:1),
- (v) "BACE1" (SEQ ID No:68),
- (vi) "BSCv protein" (SEQ ID No:70),
- (vii) "CGI-13" (SEQ ID No:72)
- (viii) "Casein kinase II beta chain" (SEQ ID No:74),
- (ix) "Cathepsin B" (SEQ ID No:75),
- (x) "ENSG00000144840" (SEQ ID No:79)
- (xi) "FLJ13977" (SEQ ID No:81),
- (xii) "FLJ20342" (SEQ ID No:56),
- (xiii) "FLJ20481" (SEQ ID No:82),
- (xiv) "FLJ22390" (SEQ ID No:84),

- (xv) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86),
- (xvi) "ICAM-2" (SEQ ID No:87)
- (xvii) "KIAA1181" (SEQ ID No:88),
- (xiii) "KIAA1533" (SEQ ID No:89),
- (xix) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91)
- (xx) "NICE-3" (SEQ ID No:58),
- (xxi) "Neurotrypsin" (SEQ ID No:92),
- (xxii) "Nicastrin" (SEQ ID No:9),
- (xxiii) "PP1, regulatory subunit 15B " (SEQ ID No:93)
- (xxiv) "Pen-2" (SEQ ID No:10)
- (xxv) "Presenilin-1" (SEQ ID No:14),
- (xxvi) "Presenilin-2" (SEQ ID No:66),
- (xxvii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94)
- (xxviii) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95)
- (xxix) "Protocadherin beta 8 " (SEQ ID No:96)
- (xxx) "REP8 protein " (SEQ ID No:97)
- (xxxi) "RING finger protein 5 " (SEQ ID No:98)
- (xxxii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99)
- (xxxiii) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100)
- (xxxiv) "Thioredoxin domain-containing protein" (SEQ ID No:101), and
- (xxxv) "Voltage-dependent anion channel 1" (SEQ ID No:102),

In a preferred embodiment, the one or more proteins of the Nicastrin (b) complex are selected from the group consisting of of

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53)
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119)
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103)
- (iv) "Aph-1a" (SEQ ID No:1)
- (v) "BACE1" (SEQ ID No:38)
- (vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70)
- (vii) "CAMK4" (SEQ ID No:104)
- (viii) "CGI-13" (SEQ ID No:72)

- (ix) "Casein kinase II beta chain" (SEQ ID No:74)
- (x) "Cathepsin B" (SEQ ID No:75)
- (xi) "DCTN1" (SEQ ID No:106)
- (xii) "ENSG00000144840" (SEQ ID No:79)
- (xiii) "FACL3" (SEQ ID No:108)
- (xiv) "FACL4" (SEQ ID No:109)
- (xv) "FLJ13977" (SEQ ID No:81)
- (xvi) "FLJ20342" (SEQ ID No:56)
- (xvii) "FLJ20481" (SEQ ID No:82)
- (xiii) "FLJ22390" (SEQ ID No:84)
- (xix) "ICAM-2" (SEQ ID No:87)
- (xx) "KIAA0095" (SEQ ID No:110)
- (xxi) "KIAA0922" (SEQ ID No:111)
- (xxii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88)
- (xxiii) "KIAA1533 (FRAGMENT)" (SEQ ID No:89)
- (xxiv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91)
- (xxv) "NICE-3" (SEQ ID No:58)
- (xxvi) "Neurotrypsin" (SEQ ID No:92)
- (xxvii) "Nicastrin" (SEQ ID No:9)
- (xxiii) "PAS domain containing serine/threonine kinase" (SEQ ID No:112)
- (xxix) "PP1, regulatory subunit 15B" (SEQ ID No:93)
- (xxx) "Pen-2" (SEQ ID No:10)
- (xxxi) "Presenilin-1" (SEQ ID No:14)
- (xxxii) "Presenilin-2" (SEQ ID No:66)
- (xxxiii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94)
- (xxxiv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95)
- (xxxv) "Protocadherin beta 8" (SEQ ID No:96)
- (xxxvi) "REP8 protein" (SEQ ID No:97)
- (xxxvii) "RING finger protein 5" (SEQ ID No:98)
- (xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99)
- (xxxix) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100)
- (xl) "Thioredoxin domain-containing protein" (SEQ ID No:101)

- (xli) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113), and
- (xlii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86),

In a preferred embodiment, the one or more proteins of the Nicastrin (c) complex are selected from the group consisting of

- (i) "APP-C99" (SEQ ID No:120)
- (ii) "Nicastrin" (SEQ ID No:9)
- (iii) "Psen1" (SEQ ID No:3)
- (iv) "aph-1a" (SEQ ID No:1)
- (v) "APP" (SEQ ID No:23)
- (vi) "CtnnA1" (SEQ ID No:47)
- (vii) "CtnnA2" (SEQ ID No:48)
- (viii) "CtnnB1" (SEQ ID No:46)
- (ix) "CtnnD1" (SEQ ID No:49)
- (x) "JUP" (SEQ ID No:2)
- (xi) "NCadh" (SEQ ID No:50)
- (xii) "ACAT1" (SEQ ID No:4)
- (xiii) "CGI-13" (SEQ ID No:72)
- (xiv) "CK2B" (SEQ ID No:59)
- (xv) "CLGN" (SEQ ID No:54)
- (xvi) "ECSIT" (SEQ ID No:55)
- (xvii) "FACL3" (SEQ ID No:11)
- (xviii) "FLJ20481" (SEQ ID No:82)
- (xix) "ITM2C" (SEQ ID No:13)
- (xx) "ITPR1" (SEQ ID No:16)
- (xxi) "KIAA0363" (SEQ ID No:105)
- (xxii) "MDR1" (SEQ ID No:18)
- (xxiii) "Neurotrypsin" (SEQ ID No:19)
- (xxiv) "PTP LOC114971" (SEQ ID No:60)
- (xxv) "RetSDR2" (SEQ ID No:21)
- (xxvi) "SFXN1" (SEQ ID No:24)

- (xxvii) "SPC18" (SEQ ID No:26)
- (xxiii) "SPC22" (SEQ ID No:27)
- (xxix) "SPC25" (SEQ ID No:28)
- (xxx) "SPTLC2" (SEQ ID No:117)
- (xxxi) "stearoyl-CoA desaturase" (SEQ ID No:29)
- (xxxii) "STT3" (SEQ ID No:61)
- (xxxiii) "TMP21" (SEQ ID No:30)
- (xxxiv) "UGCGL1" (SEQ ID No:45)
- (xxxv) "visinin-like 1" (SEQ ID No:37)
- (xxxvi) "Wolframin" (SEQ ID No:67)
- (xxxvii) "YME1L1" (SEQ ID No:32)

In a preferred embodiment, the one or more proteins of BACE1 (a) complex are selected from the group consisting of

- (i) "CGI-13" (SEQ ID No:72)
- (ii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35)
- (iii) "Calsyntenin 1" (SEQ ID No:36)
- (iv) "Delta-like homolog" (SEQ ID No:118)
- (v) "FLJ30668" (SEQ ID No:69)
- (vi) "FLJ39249" (SEQ ID No:71)
- (vii) "ITCH" (SEQ ID No:73)
- (viii) "KIAA1250" (SEQ ID No:107)
- (ix) "Nicastrin" (SEQ ID No:9)
- (x) "Nogo-A" (SEQ ID No:77)
- (xi) "PDGFRB" (SEQ ID No:78)
- (xii) "PTK7" (SEQ ID No:80)
- (xiii) "SERPINA1" (SEQ ID No:83)
- (xiv) "SIM TO Y71H10A. 2.P" (SEQ ID No:85)
- (xv) "STX10" (SEQ ID No:65)
- (xvi) "Sortilin-related receptor" (SEQ ID No:52)
- (xvii) "Thioredoxin domain-containing protein" (SEQ ID No:101)
- (xviii) "integral membrane transporter protein" (SEQ ID No:114)

- (xix) "kinectin 1 (kinesin receptor)" (SEQ ID No:90), and
- (xx) "BACE1" (SEQ ID No:38),

In a preferred embodiment, the one or more proteins of the BACE1 (b) complex are selected from the group consisting of

- (i) "APP" (SEQ ID No:23)
- (ii) "Nicastrin" (SEQ ID No:9)
- (iii) "ACAT1" (SEQ ID No:4)
- (iv) "APLP2" (SEQ ID No:22)
- (v) "BRI" (SEQ ID No:5)
- (vi) "calsyntenin 1" (SEQ ID No:6)
- (vii) "CELSR2" (SEQ ID No:39)
- (viii) "CGI-13" (SEQ ID No:72)
- (ix) "DLK1" (SEQ ID No:7)
- (x) "DSCD75" (SEQ ID No:8)
- (xi) "FADS2" (SEQ ID No:40)
- (xii) "GPR49" (SEQ ID No:115)
- (xiii) "ITM2C" (SEQ ID No:13)
- (xiv) "KiDins220" (SEQ ID No:17)
- (xv) "LAPTM4B" (SEQ ID No:33)
- (xvi) "Neurotrypsin" (SEQ ID No:19)
- (xvii) "NogoA" (SEQ ID No:41)
- (xviii) "OS-9" (SEQ ID No:42)
- (xix) "PDGFRB" (SEQ ID No:43)
- (xx) "PTK7" (SEQ ID No:44)
- (xxi) "RetSDR2" (SEQ ID No:21)
- (xxii) "S100alpha" (SEQ ID No:34)
- (xxiii) "SORL1" (SEQ ID No:25)
- (xxiv) "stearoyl-CoA desaturase" (SEQ ID No:29)
- (xxv) "TMP21" (SEQ ID No:30)
- (xxvi) "UGCGL1" (SEQ ID No:45)
- (xxvii) "BACE1" (SEQ ID No:38)

In a preferred embodiment, the one or more proteins of the Psen2-complex are selected from the group consisting of

- (i) "aph-1a" (SEQ ID No:1)
- (ii) "Nicastrin" (SEQ ID No:9)
- (iii) "CGI-13" (SEQ ID No:72)
- (iv) "DSCD75" (SEQ ID No:8)
- (v) "ECSIT" (SEQ ID No:55)
- (vi) "FACL3" (SEQ ID No:11)
- (vii) "FADS2" (SEQ ID No:40)
- (viii) "FLJ10579" (SEQ ID No:12)
- (ix) "FLJ20481" (SEQ ID No:82)
- (x) "ITPR1" (SEQ ID No:16)
- (xi) "KIAA0090" (SEQ ID No:57)
- (xii) "MDR1" (SEQ ID No:18)
- (xiii) "NicAChRa3" (SEQ ID No:62)
- (xiv) "PLD3" (SEQ ID No:20)
- (xv) "SFXN1" (SEQ ID No:24)
- (xvi) "SLC4A2" (SEQ ID No:63)
- (xvii) "SORT1" (SEQ ID No:15)
- (xviii) "SPC18" (SEQ ID No:26)
- (xix) "SPC22" (SEQ ID No:27)
- (xx) "SPC25" (SEQ ID No:28)
- (xxi) "SPTLC2" (SEQ ID No:117)
- (xxii) "stearoyl-CoA desaturase" (SEQ ID No:29)
- (xxiii) "STT3" (SEQ ID No:61)
- (xxiv) "TMP21" (SEQ ID No:30)
- (xxv) "VLCAD" (SEQ ID No:31)
- (xxvi) "Wolframin" (SEQ ID No:67)
- (xxvii) "YME1L1" (SEQ ID No:32), and
- (xxviii) "Psen2" (SEQ ID No:121)

In a preferred embodiment, the at least one protein of PTK7 complex is selected from the group consisting of

- (i) "APP" (SEQ ID No:23)
- (ii) "BRI" (SEQ ID No:5)
- (iii) "CELSR2" (SEQ ID No:39)
- (iv) "DLK1" (SEQ ID No:7)
- (v) "FADS2" (SEQ ID No:40)
- (vi) "HIFPH3/EGLN3 " (SEQ ID No:64)
- (vii) "ITM2C" (SEQ ID No:13)
- (viii) "Nap1-like " (SEQ ID No:116)
- (ix) "Reelin" (SEQ ID No:51)
- (x) "PTK7" (SEQ ID No:44)

Preferably, one or more of the proteins are present in the form a fusion protein comprising said protein fused to an amino acid sequence different from that of the protein.

In a further preferred embodiment, said amino acid sequence is an affinity tag or label.

The invention further relates to a process for preparing and optionally analyzing a complex of the invention or of one or more components thereof comprising the following steps:

Expressing a protein of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the protein, preferably a tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.

Preferably, the tagged protein comprises two different tags which allow two separate affinity purification steps. More preferred, the two tags are separated by a cleavage site for a protease.

The invention further relates to a nucleic acid construct containing one or more nucleic acids encoding proteins of a complex according to the invention and to a host cell, containing such a nucleic acid construct.

Furthermore, the invention provides a kit comprising in one container the complex of the invention, optionally together with an antibody against the complex and/or further components such as reagents and working instructions.

The invention also relates to a kit of the invention for processing a substrate of a complex of the invention.

The invention further provides the kit according to the invention for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

The invention further provides an array in which at least a complex according to the invention is attached to a solid carrier.

The invention further provides a process for processing a substrate of a complex of the invention comprising the step of bringing into contact a complex of the invention with said substrate, such that said substrate is processed.

Furthermore, the invention relates to a pharmaceutical composition comprising the protein complex of the invention.

The invention further provides this pharmaceutical composition according to the invention for the treatment of neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

Furthermore, the invention provides a method for screening for a molecule that binds to the complex of the invention, comprising the following steps:

- (a) exposing said complex, or a cell or organism containing said complex, to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex.

Furthermore, the invention is directed to a method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of claims 1 to 7 comprising the steps of:

(a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and

(b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex.

Preferably, this method of the invention further comprises the step of determining whether said candidate molecule modulates gamma secretase and/or beta-secretase modulator activity.

Preferably, the amount of said complex is determined.

In another preferred embodiment, the activity of said complex is determined, wherein preferably said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

In a preferred embodiment, the substrate is APP and the cleavage of APP is analyzed.

In a further preferred embodiment, the amount of the individual protein components of said complex is determined.

Preferably, said determining step comprises determining whether any of the proteins of the respective complex as defined above is present in the complex.

In a further preferred embodiment, said method is a method of screening for a drug for treatment or prevention of neurodegenerative disease such as Alzheimer's disease.

The invention further relates to the use of a molecule that modulates the amount of, activity of, or the protein components of the complex of the invention for the manufacture of a medicament for the treatment or prevention of a neurodegenerative disease such as Alzheimer's disease. Preferably, the modulating molecule is a FADS2 interacting molecule, preferably a FADS2 inhibitor as defined above in the other use of the invention.

The invention further relates to a method for the production of a pharmaceutical composition comprising carrying out the method as defined above and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

The invention further relates to a method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of the invention, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex.

Preferably, the activity of gamma secretase and/or beta-secretase modulator is determined or the amount of said complex is determined.

In a further preferred embodiment, the activity of said complex is determined.

Preferably, said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

Preferably the amount of the individual protein components of said complex are determined, wherein said determining step comprises determining whether any of the proteins of the complexes as defined above is present in the complex.

The invention further relates to the complex of the invention, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

Furthermore, the invention relates to a method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of the invention, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity or, or protein components of, said complex.

Preferably, the modulating molecule is a FADS2 interacting molecule, preferably a FADS2-inhibitor as defined above.

Preferably, said disease or disorder involves decreased levels of the amount or activity of said complex.

In a further preferred embodiment, said disease or disorder involves increased levels of the amount or activity of said complex.

The invention further relates to the complex of the invention as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

With respect to the complex of the invention and related methods and uses as defined above the following definitions and explanations apply:

Presenilins:

Presenilins 1 and 2 (Psen1 and Psen2, also referred to as PS1 and PS2 respectively) are integral membrane proteins which are localised in the endoplasmic reticulum, the Golgi and also at the cell surface (Kovacs, *Nat Med* 2, 224). They are predominantly found as a heterodimers of the NTF and CTF endoproteolytic fragments. The protease that cleaves presenilins (the "presenilinase") is not known, it is likely that the process is autocatalytic, also the functional significance of PS (auto)proteolysis is unclear. Presenilins are involved in the proteolytical processing of Amyloid precursor protein (APP) (De Strooper et al, *Nature* 391, 387) and the Notch receptor (De Strooper et al, *Nature* 398, 518). In addition, Presenilins are associated with the cell-adhesion proteins alpha and beta-catenin, N-cadherin, and E-cadherin (Georgakopoulos et al, *Mol Cell* 4, 893) and other members of the armadillo family (Yu et al, *J Biol Chem* 273, 16470). APP processing by Presenilins is through their effects on gamma-secretase which cleaves APP, generating the C-terminus of the A-beta peptide. PS1 associates with the C83 and C99 processed C-terminal fragments of APP (Xia et al, *Proc Natl Acad Sci USA*, 94, 8208), Nicastrin (Yu et al, *Nature* 407, 48) and Pen-2 (Francis et al, *Dev Cell* 3, 85). Aph-1 (Francis et al, *Dev Cell* 3, 85) is required in Presenilin processing. It is not clear whether Presenilins regulate gamma-secretase activity directly or whether they are protease enzymes themselves (Kopan and Gouate, *Genes Dev* 14, 2799). The gamma secretase activity could comprise a multimeric complex of these proteins (Yu et al, *Nature* 407, 48) but it is not known how the relationship between these proteins affects secretase activity.

Familial Alzheimer's disease (FAD) patients carry mutations in the presenilin proteins (PS1; PS2) or in APP. These mutations result in increased production of A-beta42 (Li and Sudhof, *J. Biol. Chem* 279, 10542) which is the main component of cerebral plaques in FAD (Vassar, *Adv Drug Deliv Rev* 54, 1589).

Understanding the composition of the gamma-secretase complex, the relationship between its component parts and its regulation are important in the design of drugs for use in Alzheimer's disease patients.

Nicastrin

Nicastrin is a type 1 trans-membrane glycoprotein with a conserved transmembrane domain and DYIGS motif (Yu et al, *Nature* 407, 48) which is constitutively expressed in neural cell lines (Sato and Kuroda, *Neuropathology* 21, 115). Biochemical studies have shown that Nicastrin binds to Presenilins 1 and 2, C-terminal derivatives of APP (Yu et al, *Nature* 407,

48), membrane-tethered forms of Notch (Chen et al, Nat Cell Biol 3, 751) and that it is a member of the gamma-secretase complex along with PS1 and PS2. It has been shown that Nicastrin is required for the intra-membrane cleavage of Notch (Lopez-Schier and St Johnston, Dev Cell 2, 79) and APP (Chung and Struhl, Nat Cell Biol 3, 1129), it may also have a role in post-translational stabilisation of Presenilin (Hu et al, Dev Cell 2, 69).

Aph-1 and Pen-2 were cloned recently in a screen for presenilin enhancers ("pen") in *C. elegans* and shown to interact genetically with Aph-2 (Nicastrin). Defects in Aph-1 affect Notch signalling and Nicastrin localization. Aph-1 and Pen-2 are required for Notch cleavage, gamma-secretase activity and the accumulation of processed Presenilins. Francis et al. cloned the putative human orthologues of these genes, Aph-1a, Aph-1b and Pen-2, and recently Lee et al. also cloned the human Aph-1 cDNAs.

The exact components of the gamma-secretase complex are not known but these two novel proteins could be components of or accessory factors to the complex and may interact together directly with Presenilin or with a Presenilin/Nicastrin complex. Nicastrin is therefore a member of the active gamma-secretase complex and there is recent evidence that it is the fully glycosylated form of the protein which is important in this complex.

BACE1 (beta-secretase)

Vassar et al. (Science 286, 735) cloned a transmembrane aspartic protease that had the characteristics of the postulated beta-secretase of APP. Three other groups also cloned BACE1 using different approaches. BACE1 knockout mice have a normal phenotype, suggesting that therapeutic inhibition of BACE1 for AD may be free of mechanism-based toxicity. BACE1 ^{-/-} mice who are also homozygous for an amyloid precursor protein transgene lack brain beta-amyloid and beta-secretase-cleaved APP C-terminal fragments. Brain and primary cortical cultures from BACE1 knockout mice showed no detectable beta-secretase activity, and primary cortical cultures from BACE knockout mice produced much less amyloid-beta from APP. This suggests that BACE1, rather than its paralogue BACE2, is the main beta-secretase for APP.

BACE1 is a protein of 501 amino acids containing a 21-aa signal peptide followed by a proprotein domain spanning aa 22 to 45. There are alternatively spliced forms, BACE-I-457 and BACE-I-476. The luminal domain of the mature protein is followed by one predicted transmembrane domain and a short cytosolic C-terminal tail of 24 aa. BACE1 is predicted to

be a type 1 transmembrane protein with the active site on the luminal side of the membrane, where beta-secretase cleaves APP and possible other yet unidentified substrates. BACE1 mRNA in rat brain is present at higher levels in neurons than in glia, supporting that neurons are the primary source of the extracellular A-beta deposited in plaques. Sequence and mass spectrometry analyses showed that asn153, asn172, asn223, and asn354 of the BACE1 ectodomain are N-glycosylation sites. In addition, the ectodomain contains 6 cys residues that form disulfide bridges between positions 216 and 420, 278 and 443, and 330 and 380. The C-terminal domain of BACE1 contains a dileucine motif (LL499/500) that can potentially regulate its trafficking and endocytosis, and an adjacent serine, which is a casein kinase 1 phosphorylation site (S498). The propeptide is predominantly cleaved from BACE1 by furin. In cells expressing wt or Swedish mutant APP, transient overexpression of BACE1 decreased alpha-secretase cleavage and increased beta-secretase activity at the known beta-secretase positions, asp1 and glu11. Although BACE1 is clearly a key enzyme required for the processing of APP into Ab, other potential substrates and functions of BACE1 are unknown. Also, no BACE1 interacting proteins with regulatory or modulatory functions have been described. Proteins that activate BACE1 activity would form suitable intervention points for Alzheimer's disease therapy. In addition, proteins that inhibit BACE1, like substrates or pseudosubstrates, could also provide suitable means of intervention e.g. as proteins therapeutics.

Protein Tyrosine Kinase 7 (PTK7)

PTK7, also referred to as colon carcinoma kinase 4 (CCK4), is an immunoglobulin superfamily transmembrane glycoprotein related to chicken KLG and D. melanogaster off-track. The gene has been mapped to human chromosome 6p21.1-->p12.2 by fluorescence in situ hybridization (Banga et al., 1997, Cytogenet Cell Genet. 1997;76(1-2):43-4).

PTK7, several splicing variants of which exist in human tissues, differs from the receptor tyrosine kinase consensus sequence in several positions, suggesting that the protein be catalytically inactive (Mossie et al., 1995, Oncogene. 1995 Nov 16;11(10):2179-84.).

PTK7 is expressed in multiple human tissues, but its function is unknown. However, its similarity to the D. melanogaster transmembrane protein Off-track/Dtrk, which serves as a coreceptor of plexin A for semaphorins Sema 1A (Winberg et al., Neuron. 2001 Oct 11;32(1):53-62) and Sema 6D (Toyofuku et al., Genes Dev. 2004 Feb 15;18(4):435-47.),

suggests that PTK7 might act as a coreceptor of a plexin-like protein. In the CNS, PTK7 might therefore play a role in maintenance of neuronal connectivity.

Said object is further achieved by the characterization of component proteins. These proteins are listed in table 2.

Furthermore, using functional assays, novel targets enabling novel therapies for the treatment of Alzheimer's disease were identified, namely FADS2, DEGS, SCD4

Fatty acid $\Delta 6$ desaturase (FADS2) has been known to catalyze the rate-limiting step in the biosynthesis of polyunsaturated fatty acids (PUFA), the conversion of either linoleic acid (C18:2) into γ -linolenic acid (gLA; C18:3n-6) in the n-6 metabolic pathway or of α -linolenic acid (aLA; C18:3n-3) into stearidonic acid (C18:4n-3) in the n-3 metabolic pathway. gLA is subsequently elongated and converted to arachidonic acid (AA; C20:4n-6) by fatty acid $\Delta 5$ desaturase (FADS1). AA is the essential precursor of various eicosanoids, such as prostaglandins and leukotrienes. In the n-3 metabolic pathway, FADS1 generates eicosapentaenoic acid (EPA; C20:5n-3), a PUFA that has been suggested to have neuroprotective effects (Lynch et al., 2003) and to be beneficial in the treatment of schizophrenia and depression (Emsley et al., 2003).

Another elongation step converts EPA into docosapentaenoic acid (DPA; C22:5n-3) and further to C24:5n-3. This PUFA and the analogous n-6 fatty acid, C24:4n-6, are additional substrates of FADS2, which converts them into C24:6n-3 and C24:5n-6, respectively. Both C24 PUFAs are partially oxidized in peroxisomes to give rise to docosahexaenoic acid (DHA; C22:6n-3), a major brain PUFA, and C22:5n-6, respectively.

Three human FADS family members have been cloned (see also for rodents (Cho et al (1999), J Biol Chem 274, 37335-37339; Marquardt, A (2000) Genomics 66, 175). All are fusion products composed of an N-terminal cytochrome b5-like domain and a C-terminal multiple membrane-spanning desaturase portion, both characterized by conserved His-motifs. FADS genes are clustered at 11q12-q13.1; likely arisen from gene duplication. The function of a related gene product, FADS3, is unknown, but given the high level of sequence similarity between FADS2 and FADS3 it has been proposed that FADS3 may constitute an alternative fatty acid $\Delta 6$ desaturase.

According to the functional assays provided herein, $\Delta 5$ desaturase (FADS1) does not have an effect on the metabolism of APP.

Thus FADS1 (SEQ ID 122) and the orthologs thereof are excluded from the scope of the invention. Those sequences are thus excluded from the general definition of homologs provided herein.

FADS3 (SEQ ID 125), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity is explicitly included within the scope of the invention as a screening tool for compounds for the treatment of Alzheimer's disease and/or the modulation of gamma-secretase-activity and/or beta-secretase activity.

In particular, the invention relates to FADS2 or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity and/or beta-secretase activity, with the proviso that FADS1 (SEQ 122) is excluded.

Furthermore, the invention relates to DEGS (SEQ ID 123) and SCD4 (SEQ ID 123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity and/or beta-secretase activity.

3.1 DEFINITIONS

The term "activity" as used herein, refers to the function of a molecule in its broadest sense. It generally includes, but is not limited to, biological, biochemical, physical or chemical functions of the molecule. It includes for example the enzymatic activity, the ability to interact with other molecules and ability to activate, facilitate, stabilize, inhibit, suppress or destabilize the function of other molecules, stability, ability to localize to certain subcellular locations. Where applicable, said term also relates to the function of a protein complex in its broadest sense.

The term "agonist" as used herein, means a molecule which modulates the formation of a protein complex or which, when bound to a complex or protein of the invention or a molecule in the protein complex, increases the amount of, or prolongs the duration of, the activity of the complex. The stimulation may be direct or indirect, including effects on the expression of a gene encoding a member of the protein complex, or by a competitive or non-competitive mechanism. Agonists may include proteins, nucleic acids, carbohydrates or any other organic or inorganic molecule or metals. Agonists also include a functional peptide or peptide fragment derived from a protein member of the complexes of the invention or a protein member itself of the complexes of the invention. Preferred activators are those which, when added to the complex and/or the protein of the invention under physiological conditions and/or in vitro assays, including diagnostic or prognostic assays, result in a change of the

level of any of the activities of the protein complex and/or the proteins of the invention as exemplary illustrated above by at least 10%, at least 25%, at least 50%, at least 100%, at least, 200%, at least 500% or at least 1000% at a concentration of the activator $1\mu\text{g ml}^{-1}$, $10\mu\text{g ml}^{-1}$, $100\mu\text{g ml}^{-1}$, $500\mu\text{g ml}^{-1}$, 1mg ml^{-1} , 10mg ml^{-1} or 100mg ml^{-1} . Any combination of the above mentioned degrees of percentages and concentration may be used to define an agonist of the invention, with greater effect at lower concentrations being preferred.

The term "amount" as used herein and as applicable to the embodiment described relates to the amount of the particular protein or protein complex described, including the value of null, i.e. where no protein or protein complex described in that particular embodiment is present under the or any of the conditions which might be specified in that particular embodiment.

The term "animal" as used herein includes, but is not limited to mammals, preferably mammals such as cows, pigs, horses, mice, rats, cats, dogs, sheep, goats and most preferably humans. Other animals used in agriculture, such as chickens, ducks etc. are also included in the definition as used herein.

The term "animal" as used herein does not include humans if being used in the context of genetic alterations to the germline.

The term "antagonist" as used herein, means a molecule which modulates the formation of a protein complex or which, when bound to a complex or protein of the invention or a molecule in the protein complex, decreases the amount of, or the duration or level of activity of the complex. The effect may be direct or indirect, including effects on the expression of a gene encoding a member of the protein complex, or by a competitive or non-competitive mechanism. Antagonists may include proteins, including antibodies, nucleic acids, carbohydrates or any other organic or inorganic molecule or metals. Antagonists also include a functional peptide or peptide fragment derived from a protein member of the complexes of the invention or a protein member itself of the complexes of the invention. Preferred antagonists are those which, when added to the complex and/or the protein of the invention under physiological conditions and/or in vitro assays, including diagnostic or prognostic assays, result in a change of the level of any of the activities of the protein complex and/or the proteins of the invention as exemplary illustrated above by at least 10%, at least 20%, at least 30%, at least 40% at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95% or at least 99% at a concentration of the inhibitor of $1\mu\text{g ml}^{-1}$, $10\mu\text{g ml}^{-1}$, $100\mu\text{g ml}^{-1}$, $500\mu\text{g ml}^{-1}$, 1mg ml^{-1} , 10mg ml^{-1} or 100mg ml^{-1} .

Any combination of the above mentioned degrees of percentages and concentration may be used to define antagonist of the invention, with greater effect at lower concentrations being preferred.

The term "antibodies" as used herein, include include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library.

The term "binding" as used herein means a stable or transient association between two molecules, including electrostatic, hydrophobic, ionic and/or hydrogen-bond interaction under physiological conditions and/or conditions being used in diagnostic or prognostic method or process or procedure.

The term "carrier" as used herein refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, including but not limited to peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered orally. Saline and aqueous dextrose are preferred carriers when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are preferably employed as liquid carriers for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsions, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the therapeutic, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

If not stated otherwise, the terms "complex" and "protein complex" are used interchangeably herein and refer to a complex of proteins that is able to perform one or more

functions of the wild type protein complex. The protein complex may or may not include and/or be associated with other molecules such as nucleic acid, such as RNA or DNA, or lipids or further cofactors or moieties selected from a metal ions, hormones, second messengers, phosphate, sugars.

A "complex" of the invention may also be part of or a unit of a larger physiological protein assembly.

If not stated otherwise, the term "compound" as used herein are include but are not limited to peptides, nucleic acids, carbohydrates, natural product extract librariesorganic molecules, preferentially small organic molecules, anorganic molecules, including but not limited to chemicals, metals and organometallic molecules.

The terms "derivatives" or "analogs of component proteins" or "variants" as used herein include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to a sequence encoding the component protein under stringent, moderately stringent, or nonstringent conditions. It means a protein which is the outcome of a modification of the naturally occurring protein, by amino acid substitutions, deletions and additions, respectively, which derivatives still exhibit the biological function of the naturally occurring protein although not necessarily to the same degree. The biological function of such proteins can e.g. be examined by suitable available in vitro assays as provided in the invention.

The term "functionally active" as used herein refers to a polypeptide, namely a fragment or derivative, having structural, regulatory, or biochemical functions of the protein according to the embodiment of which this polypeptide, namely fragment or derivative is related to.

The term "fragment" as used herein refers to a polypeptide of at least 10, 20, 30, 40 or 50 amino acids of the component protein according to the embodiment. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids.

The term "gene" as used herein refers to a nucleic acid comprising an open reading frame encoding a polypeptide of, if not stated otherwise, the present invention, including both exon and optionally intron sequences.

The terms "homologue" or "homologous gene products" as used herein mean a protein in another species, preferably mammals, which performs the same biological function as the a protein component of the complex further described herein. Such homologues are also termed "orthologous gene products". The algorithm for the detection of orthologue gene pairs from humans and mammals or other species uses the whole genome of these organisms. First, pairwise best hits are retrieved, using a full Smith-Waterman alignment of predicted proteins. To further improve reliability, these pairs are clustered with pairwise best hits involving *Drosophila melanogaster* and *C. elegans* proteins. Such analysis is given, e.g., in Nature, 2001, 409:860-921. The homologues of the proteins according to the invention can either be isolated based on the sequence homology of the genes encoding the proteins provided herein to the genes of other species by cloning the respective gene applying conventional technology and expressing the protein from such gene, or by isolating proteins of the other species by isolating the analogous complex according to the methods provided herein or to other suitable methods commonly known in the art.

The term "host cells" or, were applicable, "cells" or "hosts" as used herein is intended to be understood in a broadest sense and include, but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

It is understood that this term not only refers to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation of environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

The term "nucleic acid" as used herein refers to polynucleotides such as deoxyribonucleic acid (DNA), and, where appropriate, ribonucleic acid (RNA). They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to polynucleotides are known in the art. These include methylphosphonate and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present

invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art. Such modifications may be carried out in order to enhance the in vivo activity or lifespan of polynucleotides of the invention. Polynucleotides according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques. The polynucleotides are typically provided in isolated and/or purified form. As applicable to the embodiment being described, they include both single stranded and double-stranded polynucleotides.

The term "percent identity", as used herein, means the number of identical residues as defined by an optimal alignment using the Smith-Waterman algorithm divided by the length of the overlap multiplied by 100. The alignment is performed by the search program (Pearson, 1991, Genomics 11:635-650) with the constraint to align the maximum of both sequences.

The terms "polypeptides" and "proteins" are, where applicable, used interchangeably herein. They may be chemically modified, e.g. post-translationally modified. For example, they may be glycosylated or comprise modified amino acid residues. They may also be modified by the addition of a signal sequence to promote their secretion from a cell where the polypeptide does not naturally contain such a sequence. They may be tagged with a tag. They may be tagged with different labels which may assist in identification of the proteins in a protein complex. Polypeptides/proteins for use in the invention may be in a substantially isolated form. It will be understood that the polypeptid/protein may be mixed with carriers or diluents which will not interfere with the intended purpose of the polypeptide and still be regarded as substantially isolated. A polypeptide/protein for use in the invention may also be in a substantially purified form, in which case it will generally comprise the polypeptide in a preparation in which more than 50%, e.g. more than 80%, 90%, 95% or 99%, by weight of the polypeptide in the preparation is a polypeptide of the invention.

"Target for therapeutic drug" means that the respective protein (target) can bind the active ingredient of a pharmaceutical composition and thereby changes its biological activity in response to the drug binding.

The term "tag" as used herein is meant to be understood in its broadest sense and to include, but is not limited to any suitable enzymatic, fluorescent, or radioactive labels and suitable epitopes, including but not limited to HA-tag, Myc-tag, T7, His-tag, FLAG-tag,

Calmodulin binding proteins, glutathione-S-transferase, strep-tag, KT3-epitope, EEF-epitopes, green-fluorescent protein and variants thereof.

The term "therapeutics" as used herein, includes, but is not limited to, a protein complex of the present invention, the individual component proteins, and analogs and derivatives (including fragments); antibodies thereto; nucleic acids encoding the component protein, and analogs or derivatives thereof; component protein antisense nucleic acids, and agents that modulate complex formation and/or activity (i.e., agonists and antagonists).

The term "vector" as used herein means a nucleic acid molecule capable of transporting another nucleic acid sequence to which it has been linked. Preferred vectors are those capable of autonomous replication and/or expression of nucleic acids to which they are linked. The terms "plasmid" and "vector" are used interchangeably herein when applicable to the embodiment. However, vectors other than plasmids are also included herein. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

An object of the present invention was to identify protein complexes of the beta-amyloid precursor protein (APP) processing pathway, component proteins of the said complexes, fragments and derivatives of the component proteins, and antibodies specific to the complexes.

Furthermore, it was an object to provide novel protein targets for the screening/development of novel therapies for the treatment of Alzheimer's disease.

The present invention relates to the protein complexes including the protein FADS2, component proteins thereof. The present invention also relates to methods for use of said complexes and in particular the use of FADS2 and also the proteins DEGS and SCD4 in, inter alia, screening, diagnosis and therapy.

By applying the process according to the invention said protein complex were identified. The components are listed in table 1.

Said object is further achieved by the characterisation of component proteins. These proteins are listed in table 2.

Furthermore, the invention relates to DEGS (SEQ ID 123) and SCD4 (SEQ ID 123) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;

wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C as a screening tool for compounds for the treatment of Alzheimer's disease and/or for the modification of the gamma-secretase activity and/or beta-secretase activity.

Animal models are also provided herein.

Preferably, the protein components of the complexes described herein are all mammalian proteins. The complexes can also consist only of the respective homologues from other mammals such as mouse, rat, pig, cow, dog, monkey, sheep or horse or other species such as *D. melanogaster*, *C. elegans* or chicken. In another preferred embodiment, the complexes are a mixture of proteins from two or more species.

PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The protein complexes of the present invention and their component proteins are described in the Tables 1 - 3. The protein complexes and component proteins can be obtained by methods well known in the art for protein purification and recombinant protein expression. For example, the protein complexes of the present invention can be isolated using the TAP method described in the Example-section, *infra*, and in WO 00/09716 and Rigaut et al., 1999, *Nature Biotechnol.* 17:1030-1032, which are each incorporated by reference in their entirety. Additionally, the protein complexes can be isolated by immunoprecipitation of the component proteins and combining the immunoprecipitated proteins. The protein complexes can also be produced by recombinantly expressing the component proteins and combining the expressed proteins.

The nucleic and amino acid sequences of the component proteins of the protein complexes of the present invention are provided herein (SEQ ID NO 1 - 121) (see. Furthermore sequences of the proteins DEGS and SCD4 are provided herein (SEQ ID 123 and 124 respectively), and can be obtained by any method known in the art, e.g., by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of each sequence, and/or by cloning from a cDNA or genomic library using an oligonucleotide specific for each nucleotide sequence.

Homologues (e.g., nucleic acids encoding component proteins from other species) or other related sequences (e.g., variants, paralogs) which are members of a native cellular protein complex can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular nucleic acid sequence as a probe, using methods well known in the art for nucleic acid hybridization and cloning.

Exemplary moderately stringent hybridization conditions are as follows: prehybridization of filters containing DNA is carried out for 8 hours to overnight at 65°C in buffer composed of 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 µg/ml denatured salmon sperm DNA. Filters are hybridized for 48 hours at 65°C in prehybridization mixture containing 100 µg/ml denatured salmon sperm DNA and 5-20 X 10⁶ cpm of ³²P-labeled probe. Washing of filters is done at 37°C for 1 hour in a solution containing 2X SSC, 0.01% PVP, 0.01% Ficoll, and 0.01% BSA. This is followed by a wash in 0.1X SSC at 50 °C for 45 min before autoradiography. Alternatively, exemplary conditions of high stringency are as follows: e.g., hybridization to filter-bound DNA in 0.5 M NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & sons, Inc., New York, at p. 2.10.3). Other conditions of high stringency which may be used are well known in the art. Exemplary low stringency hybridization conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 µg/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

For recombinant expression of one or more of the proteins, the nucleic acid containing all or a portion of the nucleotide sequence encoding the protein can be inserted into an appropriate expression vector, i.e., a vector that contains the necessary elements for the transcription and translation of the inserted protein coding sequence. The necessary transcriptional and translational signals can also be supplied by the native promoter of the component protein gene, and/or flanking regions.

A variety of host-vector systems may be utilized to express the protein coding sequence. These include but are not limited to mammalian cell systems infected with virus (e.g., vaccinia virus, adenovirus, etc.); insect cell systems infected with virus (e.g., baculovirus); microorganisms such as yeast containing yeast vectors; or bacteria transformed with bacteriophage, DNA, plasmid DNA, or cosmid DNA. The expression elements of vectors vary in their strengths and specificities. Depending on the host-vector system utilized, any one of a number of suitable transcription and translation elements may be used.

In a preferred embodiment, a complex of the present invention is obtained by expressing the entire coding sequences of the component proteins in the same cell, either under the control of the same promoter or separate promoters. In yet another embodiment, a derivative, fragment or homologue of a component protein is recombinantly expressed. Preferably the derivative, fragment or homologue of the protein forms a complex with the other components of the complex, and more preferably forms a complex that binds to an anti-complex antibody. Such an antibody is further described *infra*.

Any method available in the art can be used for the insertion of DNA fragments into a vector to construct expression vectors containing a chimeric gene consisting of appropriate transcriptional/translational control signals and protein coding sequences. These methods may include *in vitro* recombinant DNA and synthetic techniques and *in vivo* recombinant techniques (genetic recombination). Expression of nucleic acid sequences encoding a component protein, or a derivative, fragment or homologue thereof, may be regulated by a second nucleic acid sequence so that the gene or fragment thereof is expressed in a host transformed with the recombinant DNA molecule(s). For example, expression of the proteins may be controlled by any promoter/enhancer known in the art. In a specific embodiment, the promoter is not native to the gene for the component protein. Promoters that may be used can be selected from among the many known in the art, and are chosen so as to be operative in the selected host cell.

In a specific embodiment, a vector is used that comprises a promoter operably linked to nucleic acid sequences encoding a component protein, or a fragment, derivative or homologue thereof, one or more origins of replication, and optionally, one or more selectable markers (e.g., an antibiotic resistance gene).

In another specific embodiment, an expression vector containing the coding sequence, or a portion thereof, of a component protein, either together or separately, is made by subcloning the gene sequences into the EcoRI restriction site of each of the three pGEX vectors (glutathione S-transferase expression vectors; Smith and Johnson, 1988, Gene 7:31-40). This allows for the expression of products in the correct reading frame.

Expression vectors containing the sequences of interest can be identified by three general approaches: (a) nucleic acid hybridization, (b) presence or absence of "marker" gene function, and (c) expression of the inserted sequences. In the first approach, coding sequences can be detected by nucleic acid hybridization to probes comprising sequences homologous and complementary to the inserted sequences. In the second approach, the recombinant vector/host system can be identified and selected based upon the presence or absence of certain "marker" functions (e.g., resistance to antibiotics, occlusion body formation in baculovirus, etc.) caused by insertion of the sequences of interest in the vector. For example, if a component protein gene, or portion thereof, is inserted within the marker gene sequence of the vector, recombinants containing the encoded protein or portion will be identified by the absence of the marker gene function (e.g., loss of β -galactosidase activity). In the third approach, recombinant expression vectors can be identified by assaying for the component protein expressed by the recombinant vector. Such assays can be based, for example, on the physical or functional properties of the interacting species in in vitro assay systems, e.g., formation of a complex comprising the protein or binding to an anti-complex antibody.

Once recombinant component protein molecules are identified and the complexes or individual proteins isolated, several methods known in the art can be used to propagate them. Using a suitable host system and growth conditions, recombinant expression vectors can be propagated and amplified in quantity. As previously described, the expression vectors or derivatives which can be used include, but are not limited to, human or animal viruses such as vaccinia virus or adenovirus; insect viruses such as baculovirus, yeast vectors; bacteriophage vectors such as lambda phage; and plasmid and cosmid vectors.

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies or processes the expressed proteins in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus expression of the genetically-engineered component proteins may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation, etc.) of proteins. Appropriate cell lines or host systems can be chosen to ensure that the desired modification and processing of the foreign protein is achieved. For example, expression in a bacterial system can be used to produce an unglycosylated core protein, while expression in mammalian cells ensures "native" glycosylation of a heterologous protein. Furthermore, different vector/host expression systems may effect processing reactions to different extents.

In other specific embodiments, a component protein or a fragment, homologue or derivative thereof, may be expressed as fusion or chimeric protein product comprising the protein, fragment, homologue, or derivative joined via a peptide bond to a heterologous protein sequence of a different protein. Such chimeric products can be made by ligating the appropriate nucleic acid sequences encoding the desired amino acids to each other by methods known in the art, in the proper coding frame, and expressing the chimeric products in a suitable host by methods commonly known in the art. Alternatively, such a chimeric product can be made by protein synthetic techniques, e.g., by use of a peptide synthesizer. Chimeric genes comprising a portion of a component protein fused to any heterologous protein-encoding sequences may be constructed.

In particular, protein component derivatives can be made by altering their sequences by substitutions, additions or deletions that provide for functionally equivalent molecules. Due to the degeneracy of nucleotide coding sequences, other DNA sequences that encode substantially the same amino acid sequence as a component gene or cDNA can be used in the practice of the present invention. These include but are not limited to nucleotide sequences comprising all or portions of the component protein gene that are altered by the substitution of different codons that encode a functionally equivalent amino acid residue within the sequence, thus producing a silent change. Likewise, the derivatives of the invention include, but are not limited to, those containing, as a primary amino acid sequence, all or part of the amino acid sequence of a component protein, including altered sequences in which functionally equivalent amino acid residues are substituted for residues within the sequence

resulting in a silent change. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity that acts as a functional equivalent, resulting in a silent alteration. Substitutes for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

In a specific embodiment, up to 1%, 2%, 5%, 10%, 15% or 20% of the total number of amino acids in the wild type protein are substituted or deleted; or 1, 2, 3, 4, 5, or 6 or up to 10 or up to 20 amino acids are inserted, substituted or deleted relative to the wild type protein.

In a specific embodiment of the invention, the nucleic acids encoding a protein component and protein components consisting of or comprising a fragment of or consisting of at least 6 (continuous) amino acids of the protein are provided. In other embodiments, the fragment consists of at least 10, 20, 30, 40, or 50 amino acids of the component protein. In specific embodiments, such fragments are not larger than 35, 100 or 200 amino acids. Derivatives or analogs of component proteins include, but are not limited, to molecules comprising regions that are substantially homologous to the component proteins, in various embodiments, by at least 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% identity over an amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to a sequence encoding the component protein under stringent, moderately stringent, or nonstringent conditions.

In a specific embodiment, proteins are provided herein, which share an identical region of 20, 30, 40, 50 or 60 contiguous amino acids of the proteins listed in table 2.

The protein component derivatives and analogs of the invention can be produced by various methods known in the art. The manipulations which result in their production can occur at the gene or protein level. For example, the cloned gene sequences can be modified by any of numerous strategies known in the art (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The sequences can be cleaved at appropriate sites with restriction endonuclease(s), followed by further enzymatic modification if desired, isolated, and ligated in vitro. In the

production of the gene encoding a derivative, homologue or analog of a component protein, care should be taken to ensure that the modified gene retains the original translational reading frame, uninterrupted by translational stop signals, in the gene region where the desired activity is encoded.

Additionally, the encoding nucleic acid sequence can be mutated *in vitro* or *in vivo*, to create and/or destroy translation, initiation, and/or termination sequences, or to create variations in coding regions and/or form new restriction endonuclease sites or destroy pre-existing ones, to facilitate further *in vitro* modification. Any technique for mutagenesis known in the art can be used, including but not limited to, chemical mutagenesis and *in vitro* site-directed mutagenesis (Hutchinson et al., 1978, *J. Biol. Chem.* 253:6551-6558), amplification with PCR primers containing a mutation, etc.

Once a recombinant cell expressing a component protein, or fragment or derivative thereof, is identified, the individual gene product or complex can be isolated and analyzed. This is achieved by assays based on the physical and/or functional properties of the protein or complex, including, but not limited to, radioactive labeling of the product followed by analysis by gel electrophoresis, immunoassay, cross-linking to marker-labeled product, etc.

The component proteins and complexes may be isolated and purified by standard methods known in the art (either from natural sources or recombinant host cells expressing the complexes or proteins), including but not restricted to column chromatography (e.g., ion exchange, affinity, gel exclusion, reversed-phase high pressure, fast protein liquid, etc.), differential centrifugation, differential solubility, or by any other standard technique used for the purification of proteins. Functional properties may be evaluated using any suitable assay known in the art.

Alternatively, once a component protein or its derivative, is identified, the amino acid sequence of the protein can be deduced from the nucleic acid sequence of the chimeric gene from which it was encoded. As a result, the protein or its derivative can be synthesized by standard chemical methods known in the art (e.g., Hunkapiller et al., 1984, *Nature* 310:105-111).

Manipulations of component protein sequences may be made at the protein level. Included within the scope of the invention is a complex in which the component proteins or derivatives and analogs that are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other

cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH_4 , acetylation, formylation, oxidation, reduction, metabolic synthesis in the presence of tunicamycin, etc.

In specific embodiments, the amino acid sequences are modified to include a fluorescent label. In another specific embodiment, the protein sequences are modified to have a heterofunctional reagent; such heterofunctional reagents can be used to crosslink the members of the complex.

In addition, complexes of analogs and derivatives of component proteins can be chemically synthesized. For example, a peptide corresponding to a portion of a component protein, which comprises the desired domain or mediates the desired activity in vitro (e.g., complex formation) can be synthesized by use of a peptide synthesizer. Furthermore, if desired, non-classical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the protein sequence.

In cases where natural products are suspected of being mutant or are isolated from new species, the amino acid sequence of a component protein isolated from the natural source, as well as those expressed in vitro, or from synthesized expression vectors in vivo or in vitro, can be determined from analysis of the DNA sequence, or alternatively, by direct sequencing of the isolated protein. Such analysis can be performed by manual sequencing or through use of an automated amino acid sequenator.

The complexes can also be analyzed by hydrophilicity analysis (Hopp and Woods, 1981, *Proc. Natl. Acad. Sci. USA* 78:3824-3828). A hydrophilicity profile can be used to identify the hydrophobic and hydrophilic regions of the proteins, and help predict their orientation in designing substrates for experimental manipulation, such as in binding experiments, antibody synthesis, etc. Secondary structural analysis can also be done to identify regions of the component proteins, or their derivatives, that assume specific structures (Chou and Fasman, 1974, *Biochemistry* 13:222-23). Manipulation, translation, secondary structure prediction, hydrophilicity and hydrophobicity profile predictions, open reading frame prediction and plotting, and determination of sequence homologies, etc., can be accomplished using computer software programs available in the art.

Other methods of structural analysis including but not limited to X-ray crystallography (Engstrom, 1974, *Biochem. Exp. Biol.* 11:7-13), mass spectroscopy and gas chromatography (Methods in Protein Science, J. Wiley and Sons, New York, 1997), and computer modeling

(Fletterick and Zoller, eds., 1986, Computer Graphics and Molecular Modeling, In: Current Communications in Molecular Biology, Cold Spring Harbor Laboratory, Cold Spring Harbor Press, New York) can also be employed.

ANTIBODIES TO PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

According to the present invention, a protein complex of the present invention comprising a first protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in third column of table 1; and a second protein, or a functionally active fragment or functionally active derivative thereof, selected from the group consisting of proteins listed in fourth column of table 1, or a functionally active fragment or functionally active derivative thereof, can be used as an immunogen to generate antibodies which immunospecifically bind such immunogen. According to the present invention, also a protein complex of the present invention can be used as an immunogen to generate antibodies which immunospecifically bind to such immunogen comprising all proteins listed in fifth column of table 1.

Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments, and an Fab expression library. In a specific embodiment, antibodies to a complex comprising human protein components are produced. In another embodiment, a complex formed from a fragment of said first protein and a fragment of said second protein, which fragments contain the protein domain that interacts with the other member of the complex, are used as an immunogen for antibody production. In a preferred embodiment, the antibody specific for the complex in that the antibody does not bind the individual protein components of the complex.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a polypeptide of the invention as an immunogen. Preferred polyclonal antibody compositions are ones that have been selected for antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred polyclonal antibody preparations are ones that contain only antibodies directed against a polypeptide or polypeptides of the invention. Particularly preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a polypeptide of the invention. In such a manner, the only

human epitope or epitopes recognized by the resulting antibody compositions raised against this immunogen will be present as part of a polypeptide or polypeptides of the invention.

The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules can be isolated from the mammal (e.g., from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. Alternatively, antibodies specific for a protein or polypeptide of the invention can be selected for (e.g., partially purified) or purified by, e.g., affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, i.e., one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those on the desired protein or polypeptide of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein or polypeptide of the invention.

At an appropriate time after immunization, e.g., when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, 1975, *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor et al., 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (Cole et al., 1985, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* 1994, Coligan et al. (eds.) John Wiley & Sons, Inc., New York, NY). Hybridoma cells producing a monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, e.g., using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody directed against a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia Recombinant Phage Antibody System, Catalog No. 27-9400-01; and the Stratagene SurfZAP Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs et al., 1991, *Bio/Technology* 9:1370-1372; Hay et al., 1992, *Hum. Antibod. Hybridomas* 3:81-85; Huse et al., 1989, *Science* 246:1275-1281; Griffiths et al., 1993, *EMBO J.* 12:725-734.

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g., Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Humanized antibodies are antibody molecules from non-human species having one or more complementarily determining regions (CDRs) from the non-human species and a framework region from a human immunoglobulin molecule. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better et al., 1988, *Science* 240:1041-1043; Liu et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu et al., 1987, *J. Immunol.* 139:3521-3526; Sun et al., 1987, *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura et al., 1987, *Canc. Res.* 47:999-1005; Wood et al., 1985, *Nature* 314:446-449; and Shaw et al.,

1988, J. Natl. Cancer Inst. 80:1553-1559); Morrison, 1985, Science 229:1202-1207; Oi et al., 1986, Bio/Techniques 4:214; U.S. Patent 5,225,539; Jones et al., 1986, Nature 321:552-525; Verhoeyan et al., 1988, Science 239:1534; and Beidler et al., 1988, J. Immunol. 141:4053-4060.

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Such antibodies can be produced, for example, using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, 1995, Int. Rev. Immunol. 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., 1994, Bio/technology 12:899-903).

Antibody fragments that contain the idiotypes of the complex can be generated by techniques known in the art. For example, such fragments include, but are not limited to, the F(ab')₂ fragment which can be produced by pepsin digestion of the antibody molecule; the Fab' fragment that can be generated by reducing the disulfide bridges of the F(ab')₂ fragment; the Fab fragment that can be generated by treating the antibody molecular with papain and a reducing agent; and Fv fragments.

In the production of antibodies, screening for the desired antibody can be accomplished by techniques known in the art, e.g., ELISA (enzyme-linked immunosorbent assay). To select antibodies specific to a particular domain of the complex, or a derivative thereof, one may assay generated hybridomas for a product that binds to the fragment of the complex, or a derivative thereof, that contains such a domain. For selection of an antibody that specifically binds a complex of the present, or a derivative, or homologue thereof, but which does not specifically bind to the individual proteins of the complex, or a derivative, or homologue thereof, one can select on the basis of positive binding to the complex and a lack of binding to the individual protein components.

Antibodies specific to a domain of the complex, or a derivative, or homologue thereof, are also provided.

The foregoing antibodies can be used in methods known in the art relating to the localization and/or quantification of the complexes of the invention, e.g., for imaging these proteins, measuring levels thereof in appropriate physiological samples (by immunoassay), in diagnostic methods, etc. This holds true also for a derivative, or homologue thereof of a complex.

In another embodiment of the invention (see *infra*), an antibody to a complex or a fragment of such antibodies containing the antibody binding domain, is a therapeutic.

DIAGNOSTIC, PROGNOSTIC, AND SCREENING USES OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The particular protein complexes and proteins of the present invention may be markers of normal physiological processes, and thus have diagnostic utility. Further, definition of particular groups of patients with elevations or deficiencies of a protein complex of the present invention, or wherein the protein complex has a change in protein component composition, can lead to new nosological classifications of diseases, furthering diagnostic ability.

Examples for diseases or disorders are neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

Detecting levels of protein complexes, or individual component proteins that form the complexes, or detecting levels of the mRNAs encoding the components of the complex, may

be used in diagnosis, prognosis, and/or staging to follow the course of a disease state, to follow a therapeutic response, etc.

A protein complex of the present invention and the individual components of the complex and a derivative, analog or subsequence thereof, encoding nucleic acids (and sequences complementary thereto), and anti-complex antibodies and antibodies directed against individual components that can form the complex, are useful in diagnostics. The foregoing molecules can be used in assays, such as immunoassays, to detect, prognose, diagnose, or monitor various conditions, diseases, and disorders characterized by aberrant levels of a complex or aberrant component composition of a complex, or monitor the treatment of such various conditions, diseases, and disorders.

In particular, such an immunoassay is carried out by a method comprising contacting a sample derived from a patient with an anti-complex antibody under conditions such that immunospecific binding can occur, and detecting or measuring the amount of any immunospecific binding by the antibody. In a specific aspect, such binding of antibody, in tissue sections, can be used to detect aberrant complex localization, or aberrant (e.g., high, low or absent) levels of a protein complex or complexes. In a specific embodiment, an antibody to the complex can be used to assay a patient tissue or serum sample for the presence of the complex, where an aberrant level of the complex is an indication of a diseased condition. By "aberrant levels" is meant increased or decreased levels relative to that present, or a standard level representing that present, in an analogous sample from a portion or fluid of the body, or from a subject not having the disorder.

The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as Western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays, complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few known in the art.

Nucleic acids encoding the components of the protein complex and related nucleic acid sequences and subsequences, including complementary sequences, can be used in hybridization assays. The nucleic acid sequences, or subsequences thereof, comprising about at least 8 nucleotides, can be used as hybridization probes. Hybridization assays can be used to detect, prognose, diagnose, or monitor conditions, disorders, or disease states associated

with aberrant levels of the mRNAs encoding the components of a complex as described, supra. In particular, such a hybridization assay is carried out by a method comprising contacting a sample containing nucleic acid with a nucleic acid probe capable of hybridizing to component protein coding DNA or RNA, under conditions such that hybridization can occur, and detecting or measuring any resulting hybridization.

In specific embodiments, diseases and disorders involving or characterized by aberrant levels of a protein complex or aberrant complex composition can be diagnosed, or its suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by determining the component protein composition of the complex, or detecting aberrant levels of a member of the complex or un-complexed component proteins or encoding nucleic acids, or functional activity including, but not restricted to, binding to an interacting partner, or by detecting mutations in component protein RNA, DNA or protein (e.g., mutations such as translocations, truncations, changes in nucleotide or amino acid sequence relative to wild-type that cause increased or decreased expression or activity of a complex, and/or component protein).

Such diseases and disorders include, but are not limited to neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

By way of example, levels of a protein complex and the individual components of a complex can be detected by immunoassay, levels of component protein RNA or DNA can be detected by hybridization assays (e.g., Northern blots, dot blots, RNase protection assays), and binding of component proteins to each other (e.g., complex formation) can be measured by binding assays commonly known in the art. Translocations and point mutations in component protein genes can be detected by Southern blotting, RFLP analysis, PCR using primers that preferably generate a fragment spanning at least most of the gene by sequencing of genomic DNA or cDNA obtained from the patient, etc.

Assays well known in the art (e.g., assays described above such as immunoassays, nucleic acid hybridization assays, activity assays, etc.) can be used to determine whether one or more particular protein complexes are present at either increased or decreased levels, or are absent, in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, as compared to the levels in samples from subjects not having such a disease or disorder, or having a predisposition to develop such a disease or disorder. Additionally, these assays can be used to determine whether the ratio of the complex to the un-complexed components of the complex, is increased or

decreased in samples from patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, as compared to the ratio in samples from subjects not having such a disease or disorder.

In the event that levels of one or more particular protein complexes (i.e., complexes formed from component protein derivatives, homologs, fragments, or analogs) are determined to be increased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder, or predisposition for a disease or disorder, can be diagnosed, have prognosis defined for, be screened for, or be monitored by detecting increased levels of the one or more protein complexes, increased levels of the mRNA that encodes one or more members of the one or more particular protein complexes, or by detecting increased complex functional activity.

Accordingly, in a specific embodiment of the present invention, diseases and disorders involving increased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting increased levels of the one or more protein complexes, the mRNA encoding both members of the complex, or complex functional activity, or by detecting mutations in the component proteins that stabilize or enhance complex formation, e.g., mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that stabilize or enhance complex formation.

In the event that levels of one or more particular protein complexes are determined to be decreased in patients suffering from a particular disease or disorder, or having a predisposition to develop such a disease or disorder, then the particular disease or disorder or predisposition for a disease or disorder can be diagnosed, have its prognosis determined, be screened for, or be monitored by detecting decreased levels of the one or more protein complexes, the mRNA that encodes one or more members of the particular one or more protein complexes, or by detecting decreased protein complex functional activity.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving decreased levels of one or more protein complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting decreased levels of the one or more protein complexes, the mRNA encoding one or more members of the one or more complexes, or complex functional activity, or by detecting mutations in the component proteins that decrease complex formation, e.g.,

mutations such as translocations in nucleic acids, truncations in the gene or protein, changes in nucleotide or amino acid sequence relative to wild-type, that decrease complex formation.

Accordingly, in a specific embodiment of the invention, diseases and disorders involving aberrant compositions of the complexes can be diagnosed, or their suspected presence can be screened for, or a predisposition to develop such disorders can be detected, by detecting the component proteins of one or more complexes, or the mRNA encoding the members of the one or more complexes.

The use of detection techniques, especially those involving antibodies against a protein complex, provides a method of detecting specific cells that express the complex or component proteins. Using such assays, specific cell types can be defined in which one or more particular protein complexes are expressed, and the presence of the complex or component proteins can be correlated with cell viability, state, health, etc.

Also embodied are methods to detect a protein complex of the present invention in cell culture models that express particular protein complexes or derivatives thereof, for the purpose of characterizing or preparing the complexes for harvest. This embodiment includes cell sorting of prokaryotes such as but not restricted to bacteria (Davey and Kell, 1996, *Microbiol. Rev.* 60:641-696), primary cultures and tissue specimens from eukaryotes, including mammalian species such as human (Steele et al., 1996, *Clin. Obstet. Gynecol.* 39:801-813), and continuous cell cultures (Orfao and Ruiz-Arguelles, 1996, *Clin. Biochem.* 29:5-9). Such isolations can be used as methods of diagnosis, described, *supra*.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation.

Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or

activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described supra. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

THERAPEUTIC USES OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

The present invention is directed to a method for treatment or prevention of various diseases and disorders by administration of a therapeutic compound (termed herein "therapeutic"). Such "therapeutics" include, but are not limited to, a protein complex of the present invention, the individual component proteins, and analogs and derivatives (including fragments) of the foregoing (e.g., as described hereinabove); antibodies thereto (as described hereinabove); nucleic acids encoding the component protein, and analogs or derivatives, thereof (e.g., as described hereinabove); component protein antisense nucleic acids, and agents that modulate complex formation and/or activity (i.e., agonists and antagonists).

The protein complexes as identified herein can be implicated in processes which are implicated in or associated with pathological conditions.

Diseases and disorders which can be treated and/or prevented and/or diagnosed by therapeutics interacting with any of the complexes provided herein are for example neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders, inflammatory diseases such as chronic inflammatory disorders, rheumatoid arthritis and inflammatory bowel disease.

These disorders are treated or prevented by administration of a therapeutic that modulates (i.e. inhibits or promotes) protein complex activity or formation or modulates its

function or composition. Diseases or disorders associated with aberrant levels of complex activity or formation, or aberrant levels or activity of the component proteins, or aberrant complex composition or a change in the function, may be treated by administration of a therapeutic that modulates complex formation or activity or by the administration of a protein complex.

Therapeutics may also be administered to modulate complex formation or activity or level thereof in a microbial organism such as yeast, fungi such as *Candida albicans* causing an infectious disease in animals or humans.

Diseases and disorders characterized by increased (relative to a subject not suffering from the disease or disorder) complex levels or activity can be treated with therapeutics that antagonize (i.e., reduce or inhibit) complex formation or activity. Therapeutics that can be used include, but are not limited to, the component proteins or an analog, derivative or fragment of the component protein; anti-complex antibodies (e.g., antibodies specific for the protein complex, or a fragment or derivative of the antibody containing the binding region thereof; nucleic acids encoding the component proteins; antisense nucleic acids complementary to nucleic acids encoding the component proteins; and nucleic acids encoding the component protein that are dysfunctional due to, e.g., a heterologous insertion within the protein coding sequence, that are used to "knockout" endogenous protein function by homologous recombination, see, e.g., Capecchi, 1989, *Science* 244:1288-1292. In one embodiment, a therapeutic is 1, 2 or more antisense nucleic acids which are complementary to 1, 2, or more nucleic acids, respectively, that encode component proteins of a complex.

In a specific embodiment of the present invention, a nucleic acid containing a portion of a component protein gene in which gene sequences flank (are both 5' and 3' to) a different gene sequence, is used as a component protein antagonist, or to promote component protein inactivation by homologous recombination (see also, Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342: 435-438). Additionally, mutants or derivatives of a component protein that has greater affinity for another component protein or the complex than wild type may be administered to compete with wild type protein for binding, thereby reducing the levels of complexes containing the wild type protein. Other therapeutics that inhibit complex function can be identified by use of known convenient *in vitro* assays, e.g., based on their ability to inhibit complex formation, or as described in Section "Assays of protein complexes/proteins of the invention and derivatives and analogs thereof", *infra*.

In specific embodiments, therapeutics that antagonize complex formation or activity are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an increased (relative to normal or desired) level of a complex, for example, in patients where complexes are overactive or overexpressed; or (2) in diseases or disorders where an *in vitro* (or *in vivo*) assay (see *infra*) indicates the utility of antagonist administration. Increased levels of a complex can be readily detected, e.g., by quantifying protein and/or RNA, by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it *in vitro* for RNA or protein levels, or structure and/or activity of the expressed complex (or the encoding mRNA). Many methods standard in the art can be thus employed including, but not limited to, immunoassays to detect complexes and/or visualize complexes (e.g., Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.), and/or hybridization assays to detect concurrent expression of component protein mRNA (e.g., Northern assays, dot blot analysis, *in situ* hybridization, etc.).

A more specific embodiment of the present invention is directed to a method of reducing complex expression (i.e., expression of the protein components of the complex and/or formation of the complex) by targeting mRNAs that express the protein moieties. RNA therapeutics currently fall within three classes, antisense species, ribozymes, or RNA aptamers (Good et al., 1997, *Gene Therapy* 4:45-54).

Antisense oligonucleotides have been the most widely used. By way of example, but not limitation, antisense oligonucleotide methodology to reduce complex formation is presented below, *infra*. Ribozyme therapy involves the administration, induced expression, etc. of small RNA molecules with enzymatic ability to cleave, bind, or otherwise inactivate specific RNAs, to reduce or eliminate expression of particular proteins (Grassi and Marini, 1996, *Annals of Medicine* 28:499-510; Gibson, 1996, *Cancer and Metastasis Reviews* 15:287-299). RNA aptamers are specific RNA ligand proteins, such as for Tat and Rev RNA (Good et al., 1997, *Gene Therapy* 4:45-54) that can specifically inhibit their translation. Aptamers specific for component proteins can be identified by many methods well known in the art, for example, by affecting the formation of a complex in the protein-protein interaction assay described, *infra*.

In another embodiment, the activity or levels of a component protein are reduced by administration of another component protein, or the encoding nucleic acid, or an antibody that

immunospecifically binds to the component protein, or a fragment or a derivative of the antibody containing the binding domain thereof.

In another aspect of the invention, diseases or disorders associated with increased levels of an component protein of the complex may be treated or prevented by administration of a therapeutic that increases complex formation if the complex formation acts to reduce or inactivate the component protein through complex formation. Such diseases or disorders can be treated or prevented by administration of one component member of the complex, administration of antibodies or other molecules that stabilize the complex, etc.

Diseases and disorders associated with underexpression of a complex, or a component protein, are treated or prevented by administration of a therapeutic that promotes (i.e., increases or supplies) complex levels and/or function, or individual component protein function. Examples of such a therapeutic include but are not limited to a complex or a derivative, analog or fragment of the complex that are functionally active (e.g., able to form a complex), un-complexed component proteins and derivatives, analogs, and fragments of un-complexed component proteins, and nucleic acids encoding the members of a complex or functionally active derivatives or fragments of the members of the complex, e.g., for use in gene therapy. In a specific embodiment, a therapeutic includes derivatives, homologs or fragments of a component protein that increase and/or stabilize complex formation. Examples of other agonists can be identified using in vitro assays or animal models, examples of which are described, *infra*.

In yet other specific embodiments of the present invention, therapeutics that promote complex function are administered therapeutically, including prophylactically, (1) in diseases or disorders involving an absence or decreased (relative to normal or desired) level of a complex, for example, in patients where a complex, or the individual components necessary to form the complex, is lacking, genetically defective, biologically inactive or underactive, or under-expressed; or (2) in diseases or disorders wherein an in vitro or in vivo assay (see, *infra*) indicates the utility of complex agonist administration. The absence or decreased level of a complex, component protein or function can be readily detected, e.g., by obtaining a patient tissue sample (e.g., from biopsy tissue) and assaying it in vitro for RNA or protein levels, structure and/or activity of the expressed complex and/or the concurrent expression of mRNA encoding the two components of the complex. Many methods standard in the art can be thus employed, including but not limited to immunoassays to detect and/or visualize a complex, or the individual components of a complex (e.g., Western blot analysis,

immunoprecipitation followed by sodium dodecyl sulfate polyacrylamide gel electrophoresis [SDS-PAGE], immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs encoding the individual protein components of a complex by detecting and/or visualizing component mRNA concurrently or separately using, e.g., Northern assays, dot blot analysis, in situ hybridization, etc.

In specific embodiments, the activity or levels of a component protein are increased by administration of another component protein of the same complex, or a derivative, homolog or analog thereof, a nucleic acid encoding the other component, or an agent that stabilizes or enhances the other component, or a fragment or derivative of such an agent.

Generally, administration of products of species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, a human complex, or derivative, homolog or analog thereof; nucleic acids encoding the members of the human complex or a derivative, homolog or analog thereof; an antibody to a human complex, or a derivative thereof; or other human agents that affect component proteins or the complex, are therapeutically or prophylactically administered to a human patient.

Preferably, suitable in vitro or in vivo assays are utilized to determine the effect of a specific therapeutic and whether its administration is indicated for treatment of the affected tissue or individual.

In various specific embodiments, in vitro assays can be carried out with representative cells of cell types involved in a patient's disorder, to determine if a therapeutic has a desired effect upon such cell types.

Compounds for use in therapy can be tested in suitable animal model systems prior to testing in humans, including, but not limited to, rats, mice, chicken, cows, monkeys, rabbits, etc. For in vivo testing, prior to administration to humans, any animal model system known in the art may be used. Additional descriptions and sources of therapeutics that can be used according to the invention are found in Sections "Protein complexes/Proteins of the invention" to "Diagnostic, prognostic and screening uses of the protein complexes/proteins of the invention" and "Pharmaceutical compositions and therapeutic/prophylactic administration" herein.

4.4.1 GENE THERAPY

In a specific embodiment of the present invention, nucleic acids comprising a sequence encoding the component proteins, or a functional derivative thereof, are administered to modulate complex activity or formation by way of gene therapy. Gene therapy refers to therapy performed by the administration of a nucleic acid to a subject. In this embodiment of the present invention, the nucleic acid expresses its encoded protein(s) that mediates a therapeutic effect by modulating complex activity or formation. Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., 1993, *Clinical Pharmacy* 12:488-505; Wu and Wu, 1991, *Biotherapy* 3:87-95; Tolstoshev, 1993, *Ann. Rev. Pharmacol. Toxicol.* 32:573-596; Mulligan, 1993, *Science* 260:926-932; Morgan and Anderson, 1993, *Ann. Rev. Biochem.* 62:191-217; and May, 1993, *TIBTECH* 11:155-215. Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al., eds., 1993, *Current Protocols in Molecular Biology*, John Wiley & Sons, NY; and Kriegler, 1990, *Gene Transfer and Expression, A Laboratory Manual*, Stockton Press, NY.

In a preferred aspect, the therapeutic comprises a nucleic acid that is part of an expression vector that expresses one or more of the component proteins, or fragments or chimeric proteins thereof, in a suitable host. In particular, such a nucleic acid has a promoter operably linked to the protein coding region(s) (or, less preferably separate promoters linked to the separate coding regions separately), said promoter being inducible or constitutive, and optionally, tissue-specific. In another particular embodiment, a nucleic acid molecule is used in which the coding sequences, and any other desired sequences, are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intra-chromosomal expression of the component protein nucleic acids (Koller and Smithies, 1989, *Proc. Natl. Acad. Sci. USA* 86:8932-8935; Zijlstra et al., 1989, *Nature* 342:435-438).

Delivery of the nucleic acid into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid-carrying vector, or indirect, in which case, cells are first transformed with the nucleic acid in vitro, then transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid is directly administered in vivo, where it is expressed to produce the encoded product. This can be accomplished by any of numerous

methods known in the art, e.g., by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by infection using a defective or attenuated retroviral or other viral vector (U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors, or through use of transfecting agents, by encapsulation in liposomes, microparticles, or microcapsules, or by administering it in linkage to a peptide that is known to enter the nucleus, or by administering it in linkage to a ligand subject to receptor-mediated endocytosis that can be used to target cell types specifically expressing the receptors (e.g., Wu and Wu, 1987, J. Biol. Chem. 262:4429-4432), etc. In another embodiment, a nucleic acid-ligand complex can be formed in which the ligand comprises a fusogenic viral peptide that disrupts endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., International Patent Publications WO 92/06180; WO 92/22635; WO 92/20316; WO 93/14188; and WO 93/20221. Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, 1989, Proc. Natl. Acad. Sci. USA 86:8932-8935; Zijlstra et al., 1989, Nature 342:435-438).

In a specific embodiment, a viral vector that contains the component protein encoding nucleic acids is used. For example, a retroviral vector can be used (Miller et al., 1993, Meth. Enzymol. 217:581-599). These retroviral vectors have been modified to delete retroviral sequences that are not necessary for packaging of the viral genome and integration into host cell DNA. The encoding nucleic acids to be used in gene therapy is/are cloned into the vector, which facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., 1994, Biotherapy 6:291-302, which describes the use of a retroviral vector to deliver the *mdr1* gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are Clowes et al., 1994, J. Clin. Invest. 93:644-651; Kiem et al., 1994, Blood 83:1467-1473; Salmons and Gunzberg, 1993, Human Gene Therapy 4:129-141; and Grossman and Wilson, 1993, Curr. Opin. in Genetics and Devel. 3:110-114.

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for

adenovirus-based delivery systems are the liver, the central nervous system, endothelial cells and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, 1993, *Curr. Opin. Genet. Devel.* 3:499-503, discuss adenovirus-based gene therapy. The use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys has been demonstrated by Bout et al., 1994, *Human Gene Therapy* 5:3-10. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., 1991, *Science* 252:431-434; Rosenfeld et al., 1992, *Cell* 68:143-155; and Mastrangeli et al., 1993, *J. Clin. Invest.* 91:225-234.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., 1993, *Proc. Soc. Exp. Biol. Med.* 204:289-300).

Another approach to gene therapy involves transferring a gene into cells in tissue culture by methods such as electroporation, lipofection, calcium phosphate-mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection to isolate those cells that have taken up and are expressing the transferred gene from those that have not. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art including, but not limited to, transfection by electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, 1993, *Meth. Enzymol.* 217:599-618; Cohen et al., 1993, *Meth. Enzymol.* 217:618-644; Cline, 1985, *Pharmac. Ther.* 29:69-92) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably, is heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. In a preferred embodiment, epithelial cells are injected, e.g., subcutaneously. In another embodiment, recombinant skin cells may be applied as a skin graft onto the patient. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells)

are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes, blood cells such as T lymphocytes, B lymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, and granulocytes, various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, a component protein encoding nucleic acid is/are introduced into the cells such that the gene or genes are expressible by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained in vitro can potentially be used in accordance with this embodiment of the present invention. Such stem cells include but are not limited to hematopoietic stem cells (HSCs), stem cells of epithelial tissues such as the skin and the lining of the gut, embryonic heart muscle cells, liver stem cells (International Patent Publication WO 94/08598), and neural stem cells (Stemple and Anderson, 1992, Cell 71:973-985).

Epithelial stem cells (ESCs), or keratinocytes, can be obtained from tissues such as the skin and the lining of the gut by known procedures (Rheinwald, 1980, Meth. Cell Biol. 2A:229). In stratified epithelial tissue such as the skin, renewal occurs by mitosis of stem cells within the germinal layer, the layer closest to the basal lamina. Similarly, stem cells within the lining of the gut provide for a rapid renewal rate of this tissue. ESCs or keratinocytes obtained from the skin or lining of the gut of a patient or donor can be grown in tissue culture (Rheinwald, 1980, Meth. Cell Bio. 2A:229; Pittelkow and Scott, 1986, Mayo Clinic Proc. 61:771). If the ESCs are provided by a donor, a method for suppression of host versus graft reactivity (e.g., irradiation, or drug or antibody administration to promote moderate immunosuppression) can also be used.

With respect to hematopoietic stem cells (HSCs), any technique that provides for the isolation, propagation, and maintenance in vitro of HSCs can be used in this embodiment of the invention. Techniques by which this may be accomplished include (a) the isolation and

establishment of HSC cultures from bone marrow cells isolated from the future host, or a donor, or (b) the use of previously established long-term HSC cultures, which may be allogeneic or xenogeneic. Non-autologous HSCs are used preferably in conjunction with a method of suppressing transplantation immune reactions between the future host and patient. In a particular embodiment of the present invention, human bone marrow cells can be obtained from the posterior iliac crest by needle aspiration (see, e.g., Kodo et al., 1984, J. Clin. Invest. 73: 1377-1384). In a preferred embodiment of the present invention, the HSCs can be made highly enriched or in substantially pure form. This enrichment can be accomplished before, during, or after long-term culturing, and can be done by any technique known in the art. Long-term cultures of bone marrow cells can be established and maintained by using, for example, modified Dexter cell culture techniques (Dexter et al., 1977, J. Cell Physiol. 91:335) or Witlock-Witte culture techniques (Witlock and Witte, 1982, Proc. Natl. Acad. Sci. USA 79:3608-3612).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription.

Additional methods can be adapted for use to deliver a nucleic acid encoding the component proteins, or functional derivatives thereof, e.g., as described in Section "Protein complexes/Proteins of the invention", supra.

USE OF ANTISENSE OLIGONUCLEOTIDES FOR SUPPRESSION OF PROTEIN COMPLEX FORMATION OR PROTEIN COMPLEX/PROTEIN ACTIVITY

In a specific embodiment of the present invention, protein complex activity and formation and protein activity is inhibited by use of antisense nucleic acids for the component proteins of the complex, that inhibit transcription and/or translation of their complementary sequence. The present invention provides the therapeutic or prophylactic use of nucleic acids of at least six nucleotides that are antisense to a gene or cDNA encoding a component protein, or a portion thereof. An "antisense" nucleic acid as used herein refers to a nucleic acid capable of hybridizing to a sequence-specific portion of a component protein RNA (preferably mRNA) by virtue of some sequence complementarity. The antisense nucleic acid may be complementary to a coding and/or noncoding region of a component protein mRNA.

Such antisense nucleic acids that inhibit complex formation or activity have utility as therapeutics, and can be used in the treatment or prevention of disorders as described supra.

The antisense nucleic acids of the invention can be oligonucleotides that are double-stranded or single-stranded, RNA or DNA, or a modification or derivative thereof, which can be directly administered to a cell, or which can be produced intracellularly by transcription of exogenous, introduced sequences.

In another embodiment, the present invention is directed to a method for inhibiting the expression of component protein nucleic acid sequences, in a prokaryotic or eukaryotic cell, comprising providing the cell with an effective amount of a composition comprising an antisense nucleic acid of the component protein, or a derivative thereof, of the invention.

The antisense nucleic acids are of at least six nucleotides and are preferably oligonucleotides, ranging from 6 to about 200 nucleotides. In specific aspects, the oligonucleotide is at least 10 nucleotides, at least 15 nucleotides, at least 100 nucleotides, or at least 200 nucleotides. The oligonucleotides can be DNA or RNA or chimeric mixtures, or derivatives or modified versions thereof, and either single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. USA 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. USA 84:648-652; International Patent Publication No. WO 88/09810) or blood-brain barrier (see, e.g., International Patent Publication No. WO 89/10134), hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6:958-976), or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5:539-549).

In a preferred aspect of the invention, an antisense oligonucleotide is provided, preferably as single-stranded DNA. The oligonucleotide may be modified at any position in its structure with constituents generally known in the art.

The antisense oligonucleotides may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl)uracil, 5-carboxymethylaminomethyl-2-thio-uridine, 5-carboxymethylaminomethyluracil, dihydrouracil, β -D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine,

7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, β -D-mannosylqueosine, 5N-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

In another embodiment, the oligonucleotide comprises at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the oligonucleotide comprises at least one modified phosphate backbone selected from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal, or an analog of the foregoing.

In yet another embodiment, the oligonucleotide is a 2'-a-anomeric oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641).

The oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization-triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. USA 85:7448-7451), etc.

In a specific embodiment, the antisense oligonucleotides comprise catalytic RNAs, or ribozymes (see, e.g., International Patent Publication No. WO 90/11364; Sarver et al., 1990, Science 247:1222-1225). In another embodiment, the oligonucleotide is a 2'-O-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analog (Inoue et al., 1987, FEBS Lett. 215:327-330).

In an alternative embodiment, the antisense nucleic acids of the invention are produced intracellularly by transcription from an exogenous sequence. For example, a vector

can be introduced in vivo such that it is taken up by a cell, within which cell the vector or a portion thereof is transcribed, producing an antisense nucleic acid (RNA) of the invention. Such a vector would contain a sequence encoding the component protein. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art to be capable of replication and expression in mammalian cells. Expression of the sequences encoding the antisense RNAs can be by any promoter known in the art to act in mammalian, preferably human, cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., 1980, *Cell* 22:787-797), the herpes thymidine kinase promoter (Wagner et al., 1981, *Proc. Natl. Acad. Sci. USA* 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, *Nature* 296:39-42), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a component protein gene, preferably a human gene. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with a component protein RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

The component protein antisense nucleic acids can be used to treat (or prevent) disorders of a cell type that expresses, or preferably overexpresses, a protein complex.

Cell types that express or overexpress component protein RNA can be identified by various methods known in the art. Such methods include, but are not limited to, hybridization with component protein-specific nucleic acids (e.g., by Northern blot hybridization, dot blot hybridization, or in situ hybridization), or by observing the ability of RNA from the cell type to be translated in vitro into the component protein by immunohistochemistry, Western blot

analysis, ELISA, etc. In a preferred aspect, primary tissue from a patient can be assayed for protein expression prior to treatment, e.g., by immunocytochemistry, in situ hybridization, or any number of methods to detect protein or mRNA expression.

Pharmaceutical compositions of the invention (see Section "Pharmaceutical compositions and therapeutic/prophylactic administration", *infra*), comprising an effective amount of a protein component antisense nucleic acid in a pharmaceutically acceptable carrier can be administered to a patient having a disease or disorder that is of a type that expresses or overexpresses a protein complex of the present invention.

The amount of antisense nucleic acid that will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. Where possible, it is desirable to determine the antisense cytotoxicity *in vitro*, and then in useful animal model systems, prior to testing and use in humans.

In a specific embodiment, pharmaceutical compositions comprising antisense nucleic acids are administered via liposomes, microparticles, or microcapsules. In various embodiments of the invention, it may be useful to use such compositions to achieve sustained release of the antisense nucleic acids. In a specific embodiment, it may be desirable to utilize liposomes targeted via antibodies to specific identifiable central nervous system cell types (Leonetti et al., 1990, *Proc. Natl. Acad. Sci. U.S.A.* 87:2448-2451; Renneisen et al., 1990, *J. Biol. Chem.* 265:16337-16342).

ASSAYS OF PROTEIN COMPLEXES/PROTEINS OF THE INVENTION AND DERIVATIVES AND ANALOGS THEREOF

The functional activity of a protein complex of the present invention, or a derivative, fragment or analog thereof or protein component thereof, can be assayed by various methods. Potential modulators (e.g., agonists and antagonists) of complex activity or formation, e.g., anti-complex antibodies and antisense nucleic acids, can be assayed for the ability to modulate complex activity or formation.

In one embodiment of the present invention, where one is assaying for the ability to bind or compete with a wild-type complex for binding to an anti-complex antibody, various immunoassays known in the art can be used, including but not limited to competitive and non-competitive assay systems using techniques such as radioimmunoassay, ELISA (enzyme

linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitin reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels), western blot analysis, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

The expression of the component protein genes (both endogenous and those expressed from cloned DNA containing the genes) can be detected using techniques known in the art, including but not limited to Southern hybridization (Southern, 1975, *J. Mol. Biol.* 98:503-517), northern hybridization (see, e.g., Freeman et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:4094-4098), restriction endonuclease mapping (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2nd Ed. Cold Spring Harbor Laboratory Press, New York), RNase protection assays (*Current Protocols in Molecular Biology*, John Wiley and Sons, New York, 1997), DNA sequence analysis, and polymerase chain reaction amplification (PCR; U.S. Patent Nos. 4,683,202, 4,683,195, and 4,889,818; Gyllenstein et al., 1988, *Proc. Natl. Acad. Sci. USA* 85:7652-7657; Ochman et al., 1988, *Genetics* 120:621-623; Loh et al., 1989, *Science* 243:217-220) followed by Southern hybridization with probes specific for the component protein genes, in various cell types. Methods of amplification other than PCR commonly known in the art can be employed. In one embodiment, Southern hybridization can be used to detect genetic linkage of component protein gene mutations to physiological or pathological states. Various cell types, at various stages of development, can be characterized for their expression of component proteins at the same time and in the same cells. The stringency of the hybridization conditions for northern or Southern blot analysis can be manipulated to ensure detection of nucleic acids with the desired degree of relatedness to the specific probes used. Modifications to these methods and other methods commonly known in the art can be used.

Derivatives (e.g., fragments), homologs and analogs of one component protein can be assayed for binding to another component protein in the same complex by any method known in the art, for example the modified yeast matrix mating test described in Section "Screening

for modulators of the protein complexes/proteins of the invention" *infra*, immunoprecipitation with an antibody that binds to the component protein complexed with other component proteins in the same complex, followed by size fractionation of the immunoprecipitated proteins (e.g., by denaturing or nondenaturing polyacrylamide gel electrophoresis), Western blot analysis, etc.

One embodiment of the invention provides a method for screening a derivative, homolog or analog of a component protein for biological activity comprising contacting said derivative, homolog or analog of the component protein with the other component proteins in the same complex; and detecting the formation of a complex between said derivative, homolog or analog of the component protein and the other component proteins; wherein detecting formation of said complex indicates that said derivative, homolog or analog of has biological (e.g., binding) activity.

The invention also provides methods of modulating the activity of a component protein that can participate in a protein complex by administration of a binding partner of that protein or derivative, homolog or analog thereof.

In a specific embodiment of the present invention, a protein complex of the present invention is administered to treat or prevent a disease or disorder, since the complex and/or component proteins have been implicated in the disease and disorder. Accordingly, a protein complex or a derivative, homolog, analog or fragment thereof, nucleic acids encoding the component proteins, anti-complex antibodies, and other modulators of protein complex activity, can be tested for activity in treating or preventing a disease or disorder in *in vitro* and *in vivo* assays.

In one embodiment, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by contacting cultured cells that exhibit an indicator of the disease *in vitro*, with the therapeutic, and comparing the level of said indicator in the cells contacted with the therapeutic, with said level of said indicator in cells not so contacted, wherein a lower level in said contacted cells indicates that the therapeutic has activity in treating or preventing the disease.

In another embodiment of the invention, a therapeutic of the invention can be assayed for activity in treating or preventing a disease by administering the therapeutic to a test animal that is predisposed to develop symptoms of a disease, and measuring the change in said symptoms of the disease after administration of said therapeutic, wherein a reduction in the severity of the symptoms of the disease or prevention of the symptoms of the disease

indicates that the therapeutic has activity in treating or preventing the disease. Such a test animal can be any one of a number of animal models known in the art for disease. These animal models are well known in the art. These animal models include, but are not limited to those which are listed in the section "Screening for modulators of the protein complexes/proteins of the invention" (infra) as exemplary animal models to study any of the complexes provided in the invention.

SCREENING FOR MODULATORS OF THE PROTEIN COMPLEXES/PROTEINS OF THE INVENTION

A complex of the present invention, the component proteins of the complex and nucleic acids encoding the component proteins, as well as derivatives and fragments of the amino and nucleic acids, can be used to screen for compounds that bind to, or modulate the amount of, activity of, or protein component composition of, said complex, and thus, have potential use as modulators, i.e., agonists or antagonists, of complex activity, and/or complex formation, i.e., the amount of complex formed, and/or protein component composition of the complex.

Thus, the present invention is also directed to methods for screening for molecules that bind to, or modulate the function of, amount of, activity of, formation of or protein component composition of, a complex of the present invention. In one embodiment of the invention, the method for screening for a molecule that modulates directly or indirectly the function, activity or formation of a complex of the present invention comprises exposing said complex, or a cell or organism containing the complex machinery, to one or more candidate molecules under conditions conducive to modulation; and determining the amount of, the biochemical activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependend on the complex and/or the abundance and/or activity of a protein or protein complex dependend on the function of the complex and/or product of a gene dependend on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependend on the complex and/or the abundance and/or activity of a protein or protein complex dependend on

the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

In a further specific embodiment, a modulation of the formation process of a complex can be determined.

Such a modulation can either be a change in the typical time course of its formation or a change in the typical steps leading to the formation of the complete complex.

Such changes can for example be detected by analysing and comparing the process of complex formation in untreated wild type cells of a particular type and/or cells showing or having the predisposition to develop a certain disease phenotype and/or cells which have been treated with particular conditions and/or particular agents in a particular situation.

Methods to study such changes in time course are well known in the art and include for example Western-blot analysis of the proteins in the complex isolated at different steps of its formation.

Furthermore an aberrant intracellular localization of the protein complex and/or an aberrant transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or a gene dependent on the complex can serve as a marker for a disease and thus have diagnostic utility for any disease which is caused by an aberrant activity, function, composition or formation of the complex of the invention.

Methods to study the intracellular localization are well known in the art and include, but are not limited to immunofluorescence analysis using antibodies specific for components of the protein. Preferentially, double-stainings including staining of other cellular structures are being used to facilitate the detection of the intracellular localization. Methods to analyse the transcription levels of a gene dependent on the complex are also well known in the art and include Northern blot analysis, quantitative PCR etc. The abundance of proteins dependent on the protein can be analyzed as described supra. Methods to study changes in the activity of proteins dependent on complex depend on the protein. The choice of such methods will be apparent to any person skilled in the art.

In another embodiment, the present invention further relates to a process for the identification and/or preparation of an effector of the complex comprising the step of bringing into contact a product of any of claims 1 to 8 with a compound, a mixture or a library of compounds and determining whether the compound or a certain compound of the mixture or

library binds to the product and/or effects the products biological activity and optionally further purifying the compound positively tested as effector.

In another embodiment, the present invention is directed to a method for screening for a molecule that binds a protein complex of the present invention comprising exposing said complex, or a cell or organism containing the complex machinery, to one or more candidate molecules; and determining whether said complex is bound by any of said candidate molecules. Such screening assays can be carried out using cell-free and cell-based methods that are commonly known in the art *in vitro*, *in vivo* or *ex vivo*. For example, an isolated complex can be employed, or a cell can be contacted with the candidate molecule and the complex can be isolated from such contacted cells and the isolated complex can be assayed for activity or component composition. In another example, a cell containing the complex can be contacted with the candidate molecule and the levels of the complex in the contacted cell can be measured. Additionally, such assays can be carried out in cells recombinantly expressing a component protein from the third column of table 1, or a functionally active fragment or functionally active derivative thereof, and a component protein from fourth column of table 1, or a functionally active fragment or functionally active derivative thereof. Additionally, such assays can also be carried out in cells recombinantly expressing all component proteins from the group of proteins in the fifth column of table 1.

For example, assays can be carried out using recombinant cells expressing the protein components of a complex, to screen for molecules that bind to, or interfere with, or promote complex activity or formation. In preferred embodiments, polypeptide derivatives that have superior stabilities but retain the ability to form a complex (e.g., one or more component proteins modified to be resistant to proteolytic degradation in the binding assay buffers, or to be resistant to oxidative degradation), are used to screen for modulators of complex activity or formation. Such resistant molecules can be generated, e.g., by substitution of amino acids at proteolytic cleavage sites, the use of chemically derivatized amino acids at proteolytic susceptible sites, and the replacement of amino acid residues subject to oxidation, i.e. methionine and cysteine.

A particular aspect of the present invention relates to identifying molecules that inhibit or promote formation or degradation of a complex of the present invention, e.g., using the method described for isolating the complex and identifying members of the complex using the TAP assay described in the Example-Section, *infra*, and in WO 00/09716 and Rigaut et al.,

1999, *Nature Biotechnol.* 17:1030-1032, which are each incorporated by reference in their entirety.

In another embodiment of the invention, a modulator is identified by administering a candidate molecule to a transgenic non-human animal expressing the complex component proteins from promoters that are not the native promoters of the respective proteins, more preferably where the candidate molecule is also recombinantly expressed in the transgenic non-human animal. Alternatively, the method for identifying such a modulator can be carried out in vitro, preferably with a purified complex, and a purified candidate molecule.

Agents/molecules (candidate molecules) to be screened can be provided as mixtures of a limited number of specified compounds, or as compound libraries, peptide libraries and the like. Agents/molecules to be screened may also include all forms of antisera, antisense nucleic acids, etc., that can modulate complex activity or formation. Exemplary candidate molecules and libraries for screening are set forth in Section "Candidate molecules", *infra*.

Screening the libraries can be accomplished by any of a variety of commonly known methods. See, e.g., the following references, which disclose screening of peptide libraries: Parmley and Smith, 1989, *Adv. Exp. Med. Biol.* 251:215-218; Scott and Smith, 1990, *Science* 249:386-390; Fowlkes et al., 1992, *BioTechniques* 13:422-427; Oldenburg et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:5393-5397; Yu et al., 1994, *Cell* 76:933-945; Staudt et al., 1988, *Science* 241:577-580; Bock et al., 1992, *Nature* 355:564-566; Tuerk et al., 1992, *Proc. Natl. Acad. Sci. USA* 89:6988-6992; Ellington et al., 1992, *Nature* 355:850-852; U.S. Patent No. 5,096,815, U.S. Patent No. 5,223,409, and U.S. Patent No. 5,198,346, all to Ladner et al.; Rebar and Pabo, 1993, *Science* 263:671-673; and International Patent Publication No. WO 94/18318.

In a specific embodiment, screening can be carried out by contacting the library members with a complex immobilized on a solid phase, and harvesting those library members that bind to the protein (or encoding nucleic acid or derivative). Examples of such screening methods, termed "panning" techniques, are described by way of example in Parmley and Smith, 1988, *Gene* 73:305-318; Fowlkes et al., 1992, *BioTechniques* 13:422-427; International Patent Publication No. WO 94/18318; and in references cited hereinabove.

In a specific embodiment, fragments and/or analogs of protein components of a complex, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex formation (amount of complex or composition of complex) or activity in the cell, which thereby inhibit complex activity or formation in the cell.

In one embodiment, agents that modulate (i.e., antagonize or agonize) complex activity or formation can be screened for using a binding inhibition assay, wherein agents are screened for their ability to modulate formation of a complex under aqueous, or physiological, binding conditions in which complex formation occurs in the absence of the agent to be tested. Agents that interfere with the formation of complexes of the invention are identified as antagonists of complex formation. Agents that promote the formation of complexes are identified as agonists of complex formation. Agents that completely block the formation of complexes are identified as inhibitors of complex formation.

Methods for screening may involve labeling the component proteins of the complex with radioligands (e.g., ^{125}I or ^3H), magnetic ligands (e.g., paramagnetic beads covalently attached to photobiotin acetate), fluorescent ligands (e.g., fluorescein or rhodamine), or enzyme ligands (e.g., luciferase or β -galactosidase). The reactants that bind in solution can then be isolated by one of many techniques known in the art, including but not restricted to, co-immunoprecipitation of the labeled complex moiety using antisera against the unlabeled binding partner (or labeled binding partner with a distinguishable marker from that used on the second labeled complex moiety), immunoaffinity chromatography, size exclusion chromatography, and gradient density centrifugation. In a preferred embodiment, the labeled binding partner is a small fragment or peptidomimetic that is not retained by a commercially available filter. Upon binding, the labeled species is then unable to pass through the filter, providing for a simple assay of complex formation.

Methods commonly known in the art are used to label at least one of the component members of the complex. Suitable labeling methods include, but are not limited to, radiolabeling by incorporation of radiolabeled amino acids, e.g., ^3H -leucine or ^{35}S -methionine, radiolabeling by post-translational iodination with ^{125}I or ^{131}I using the chloramine T method, Bolton-Hunter reagents, etc., or labeling with ^{32}P using phosphorylase and inorganic radiolabeled phosphorous, biotin labeling with photobiotin-acetate and sunlamp exposure, etc. In cases where one of the members of the complex is immobilized, e.g., as described *infra*, the free species is labeled. Where neither of the interacting species is immobilized, each can be labeled with a distinguishable marker such that isolation of both moieties can be followed to provide for more accurate quantification, and to distinguish the formation of homomeric from heteromeric complexes. Methods that utilize accessory proteins that bind to one of the modified interactants to improve the sensitivity of detection, increase the stability of the complex, etc., are provided.

Typical binding conditions are, for example, but not by way of limitation, in an aqueous salt solution of 10-250 mM NaCl, 5-50 mM Tris-HCl, pH 5-8, and 0.5% Triton X-100 or other detergent that improves specificity of interaction. Metal chelators and/or divalent cations may be added to improve binding and/or reduce proteolysis. Reaction temperatures may include 4, 10, 15, 22, 25, 35, or 42 degrees Celsius, and time of incubation is typically at least 15 seconds, but longer times are preferred to allow binding equilibrium to occur. Particular complexes can be assayed using routine protein binding assays to determine optimal binding conditions for reproducible binding.

The physical parameters of complex formation can be analyzed by quantification of complex formation using assay methods specific for the label used, e.g., liquid scintillation counting for radioactivity detection, enzyme activity for enzyme-labeled moieties, etc. The reaction results are then analyzed utilizing Scatchard analysis, Hill analysis, and other methods commonly known in the arts (see, e.g., *Proteins, Structures, and Molecular Principles*, 2nd Edition (1993) Creighton, Ed., W.H. Freeman and Company, New York).

In a second common approach to binding assays, one of the binding species is immobilized on a filter, in a microtiter plate well, in a test tube, to a chromatography matrix, etc., either covalently or non-covalently. Proteins can be covalently immobilized using any method well known in the art, for example, but not limited to the method of Kadonaga and Tjian, 1986, *Proc. Natl. Acad. Sci. USA* 83:5889-5893, i.e., linkage to a cyanogen-bromide derivatized substrate such as CNBr-Sepharose 4B (Pharmacia). Where needed, the use of spacers can reduce steric hindrance by the substrate. Non-covalent attachment of proteins to a substrate include, but are not limited to, attachment of a protein to a charged surface, binding with specific antibodies, binding to a third unrelated interacting protein, etc.

Assays of agents (including cell extracts or a library pool) for competition for binding of one member of a complex (or derivatives thereof) with another member of the complex labeled by any means (e.g., those means described above) are provided to screen for competitors or enhancers of complex formation.

In specific embodiments, blocking agents to inhibit non-specific binding of reagents to other protein components, or absorptive losses of reagents to plastics, immobilization matrices, etc., are included in the assay mixture. Blocking agents include, but are not restricted to bovine serum albumin, β -casein, nonfat dried milk, Denhardt's reagent, Ficoll, polyvinylpyrrolidone, nonionic detergents (NP40, Triton X-100, Tween 20, Tween 80, etc.),

ionic detergents (e.g., SDS, LDS, etc.), polyethylene glycol, etc. Appropriate blocking agent concentrations allow complex formation.

After binding is performed, unbound, labeled protein is removed in the supernatant, and the immobilized protein retaining any bound, labeled protein is washed extensively. The amount of bound label is then quantified using standard methods in the art to detect the label as described, *supra*.

In another specific embodiments screening for modulators of the protein complexes/protein as provided herein can be carried out by attaching those and/or the antibodies as provided herein to a solid carrier. In a further specific embodiment, the invention relates to an array of said molecules.

The preparation of such an array containing different types of proteins, including antibodies) is well known in the art and is apparent to a person skilled in the art (see e.g. Ekins et al., 1989, *J. Pharm. Biomed. Anal.* 7:155-168; Mitchell et al. 2002, *Nature Biotechnol.* 20:225-229; Petricoin et al., 2002, *Lancet* 359:572-577; Templin et al., 2001, *Trends Biotechnol.* 20:160-166; Wilson and Nock, 2001, *Curr. Opin. Chem. Biol.* 6:81-85; Lee et al., 2002 *Science* 295:1702-1705; MacBeath and Schreiber, 2000, *Science* 289:1760; Blawas and Reichert, 1998, *Biomaterials* 19:595; Kane et al., 1999, *Biomaterials* 20:2363; Chen et al., 1997, *Science* 276:1425; Vaughan et al., 1996, *Nature Biotechnol.* 14:309-314; Mahler et al., 1997, *Immunotechnology* 3:31-43; Roberts et al., 1999, *Curr. Opin. Chem. Biol.* 3:268-273; Nord et al., 1997, *Nature Biotechnol.* 15:772-777; Nord et al., 2001, *Eur. J. Biochem.* 268:4269-4277; Brody and Gold, 2000, *Rev. Mol. Biotechnol.* 74:5-13; Karlstroem and Nygren, 2001, *Anal. Biochem.* 295:22-30; Nelson et al., 2000, *Electrophoresis* 21:1155-1163; Honore et al., 2001, *Expert Rev. Mol. Diagn.* 3:265-274; Albala, 2001, *Expert Rev. Mol. Diagn.* 2:145-152, Figeys and Pinto, 2001, *Electrophoresis* 2:208-216 and references in the publications listed here).

Complexes can be attached to an array by different means as will be apparent to a person skilled in the art. Complexes can for example be added to the array via a TAP-tag (as described in WO/0009716 and in Rigaut et al., 1999, *Nature Biotechnol.* 10:1030-1032) after the purification step or by another suitable purification scheme as will be apparent to a person skilled in the art.

Optionally, the proteins of the complex can be cross-linked to enhance the stability of the complex. Different methods to cross-link proteins are well known in the art. Reactive end-

groups of cross-linking agents include but are not limited to -COOH, -SH, -NH₂ or N-oxy-succinamate.

The spacer of the cross-linking agent should be chosen with respect to the size of the complex to be cross-linked. For small protein complexes, comprising only a few proteins, relatively short spacers are preferable in order to reduce the likelihood of cross-linking separate complexes in the reaction mixture. For larger protein complexes, additional use of larger spacers is preferable in order to facilitate cross-linking between proteins within the complex.

It is preferable to check the success-rate of cross-linking before linking the complex to the carrier.

As will be apparent to a person skilled in the art, the optimal rate of cross-linking need to be determined on a case by case basis. This can be achieved by methods well known in the art, some of which are exemplary described below.

A sufficient rate of cross-linking can be checked f.e. by analysing the cross-linked complex vs. a non-cross-linked complex on a denaturing protein gel.

If cross-linking has been performed successfully, the proteins of the complex are expected to be found in the same lane, whereas the proteins of the non-cross-linked complex are expected to be separated according to their individual characteristics. Optionally the presence of all proteins of the complex can be further checked by peptide-sequencing of proteins in the respective bands using methods well known in the art such as mass spectrometry and/or Edman degradation.

In addition, a rate of crosslinking which is too high should also be avoided. If cross-linking has been carried out too extensively, there will be an increasing amount of cross-linking of the individual protein complex, which potentially interferes with a screening for potential binding partners and/or modulators etc. using the arrays.

The presence of such structures can be determined by methods well known in the art and include e.g. gel-filtration experiments comparing the gel filtration profile solutions containing cross-linked complexes vs. uncross-linked complexes.

Optionally, functional assays as will be apparent to a person skilled in the art, some of which are exemplarily provided herein, can be performed to check the integrity of the complex.

Alternatively, members of the protein complex can be expressed as a single fusion protein and coupled to the matrix as will be apparent to a person skilled in the art.

Optionally, the attachment of the complex or proteins or antibody as outlined above can be further monitored by various methods apparent to a person skilled in the art. Those include, but are not limited to surface plasmon resonance (see e.g. McDonnel, 2001, *Curr. Opin. Chem. Biol.* 5:572-577; Lee, 2001, *Trends Biotechnol.* 19:217-222; Weinberger et al., 2000, 1:395-416; Pearson et al., 2000, *Ann. Clin. Biochem.* 37:119-145; Vely et al., 2000, *Methods Mol. Biol.* 121:313-321; Slepak, 2000, *J. Mol. Recognit.* 13:20-26.

Exemplary assays useful for measuring the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, BACE1-complex, PTK7-complex, include but are not limited to those described in Vassar R et al., 1999, *Science*, 286:735-41.

Exemplary assays useful for measuring the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, BACE1-complex, PTK7-complex include but are not limited to those described in Yan R et al., 1999, *Nature*, 402:533-7.

Exemplary assays useful for measuring the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, BACE1-complex, PTK7-complex include but are not limited to those described in Tian G et al., 2002, *J Biol Chem*, 277:31499-505.

Exemplary assays useful for measuring transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) of the Presenilin 2 complex, Nicastrin complex, PTK7-complex, BACE1-complex, include but are not limited to those described in Cao X et al., 2001, *Science*, 293:115-20.

CANDIDATE MOLECULES

Any molecule known in the art can be tested for its ability to modulate (increase or decrease) the amount of, activity of, or protein component composition of a complex of the present invention as detected by a change in the amount of, activity of, or protein component composition of, said complex. By way of example, a change in the amount of the complex can be detected by detecting a change in the amount of the complex that can be isolated from a cell expressing the complex machinery. For identifying a molecule that modulates complex activity, candidate molecules can be directly provided to a cell expressing the complex machinery, or, in the case of candidate proteins, can be provided by providing their encoding nucleic acids under conditions in which the nucleic acids are recombinantly expressed to produce the candidate proteins within the cell expressing the complex machinery, the complex is then isolated from the cell and the isolated complex is assayed for activity using methods well known in the art, not limited to those described, *supra*.

This embodiment of the invention is well suited to screen chemical libraries for molecules which modulate, e.g., inhibit, antagonize, or agonize, the amount of, activity of, or protein component composition of the complex. The chemical libraries can be peptide libraries, peptidomimetic libraries, chemically synthesized libraries, recombinant, e.g., phage display libraries, and in vitro translation-based libraries, other non-peptide synthetic organic libraries, etc.

Exemplary libraries are commercially available from several sources (ArQule, Tripos/PanLabs, ChemDesign, Pharmacopoeia). In some cases, these chemical libraries are generated using combinatorial strategies that encode the identity of each member of the library on a substrate to which the member compound is attached, thus allowing direct and immediate identification of a molecule that is an effective modulator. Thus, in many combinatorial approaches, the position on a plate of a compound specifies that compound's composition. Also, in one example, a single plate position may have from 1-20 chemicals that can be screened by administration to a well containing the interactions of interest. Thus, if modulation is detected, smaller and smaller pools of interacting pairs can be assayed for the modulation activity. By such methods, many candidate molecules can be screened.

Many diversity libraries suitable for use are known in the art and can be used to provide compounds to be tested according to the present invention. Alternatively, libraries can be constructed using standard methods. Chemical (synthetic) libraries, recombinant expression libraries, or polysome-based libraries are exemplary types of libraries that can be used.

The libraries can be constrained or semirigid (having some degree of structural rigidity), or linear or unconstrained. The library can be a cDNA or genomic expression library, random peptide expression library or a chemically synthesized random peptide library, or non-peptide library. Expression libraries are introduced into the cells in which the assay occurs, where the nucleic acids of the library are expressed to produce their encoded proteins.

In one embodiment, peptide libraries that can be used in the present invention may be libraries that are chemically synthesized *in vitro*. Examples of such libraries are given in Houghten et al., 1991, *Nature* 354:84-86, which describes mixtures of free hexapeptides in which the first and second residues in each peptide were individually and specifically defined; Lam et al., 1991, *Nature* 354:82-84, which describes a "one bead, one peptide" approach in which a solid phase split synthesis scheme produced a library of peptides in which each bead in the collection had immobilized thereon a single, random sequence of amino acid residues; Medynski, 1994, *Bio/Technology* 12:709-710, which describes split synthesis and T-bag synthesis methods; and Gallop et al., 1994, *J. Med. Chem.* 37:1233-1251. Simply by way of other examples, a combinatorial library may be prepared for use, according to the methods of Ohlmeyer et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:10922-10926; Erb et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:11422-11426; Houghten et al., 1992, *Biotechniques* 13:412; Jayawickreme et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:1614-1618; or Salmon et al., 1993, *Proc. Natl. Acad. Sci. USA* 90:11708-11712. PCT Publication No. WO 93/20242 and Brenner and Lerner, 1992, *Proc. Natl. Acad. Sci. USA* 89:5381-5383 describe "encoded combinatorial chemical libraries," that contain oligonucleotide identifiers for each chemical polymer library member.

In a preferred embodiment, the library screened is a biological expression library that is a random peptide phage display library, where the random peptides are constrained (e.g., by virtue of having disulfide bonding).

Further, more general, structurally constrained, organic diversity (e.g., nonpeptide) libraries, can also be used. By way of example, a benzodiazepine library (see e.g., Bunin et al., 1994, *Proc. Natl. Acad. Sci. USA* 91:4708-4712) may be used.

Conformationally constrained libraries that can be used include but are not limited to those containing invariant cysteine residues which, in an oxidizing environment, cross-link by disulfide bonds to form cystines, modified peptides (e.g., incorporating fluorine, metals, isotopic labels, are phosphorylated, etc.), peptides containing one or more non-naturally

occurring amino acids, non-peptide structures, and peptides containing a significant fraction of γ -carboxyglutamic acid.

Libraries of non-peptides, e.g., peptide derivatives (for example, that contain one or more non-naturally occurring amino acids) can also be used. One example of these are peptoid libraries (Simon et al., 1992, Proc. Natl. Acad. Sci. USA 89:9367-9371). Peptoids are polymers of non-natural amino acids that have naturally occurring side chains attached not to the α carbon but to the backbone amino nitrogen. Since peptoids are not easily degraded by human digestive enzymes, they are advantageously more easily adaptable to drug use. Another example of a library that can be used, in which the amide functionalities in peptides have been permethylated to generate a chemically transformed combinatorial library, is described by Ostresh et al., 1994, Proc. Natl. Acad. Sci. USA 91:11138-11142).

The members of the peptide libraries that can be screened according to the invention are not limited to containing the 20 naturally occurring amino acids. In particular, chemically synthesized libraries and polysome based libraries allow the use of amino acids in addition to the 20 naturally occurring amino acids (by their inclusion in the precursor pool of amino acids used in library production). In specific embodiments, the library members contain one or more non-natural or non-classical amino acids or cyclic peptides. Non-classical amino acids include but are not limited to the D-isomers of the common amino acids, γ -amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid; ϵ -Abu, ϵ -Ahx, 6-amino hexanoic acid; Aib, 2-amino isobutyric acid; 3-amino propionic acid; ornithine; norleucine; norvaline, hydroxyproline, sarcosine, citrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, β -alanine, designer amino acids such as β -methyl amino acids, C-methyl amino acids, N-methyl amino acids, fluoro-amino acids and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

In a specific embodiment, fragments and/or analogs of complexes of the invention, or protein components thereof, especially peptidomimetics, are screened for activity as competitive or non-competitive inhibitors of complex activity or formation.

In another embodiment of the present invention, combinatorial chemistry can be used to identify modulators of the complexes. Combinatorial chemistry is capable of creating libraries containing hundreds of thousands of compounds, many of which may be structurally similar. While high throughput screening programs are capable of screening these vast libraries for affinity for known targets, new approaches have been developed that achieve

libraries of smaller dimension but which provide maximum chemical diversity. (See e.g., Matter, 1997, *J. Med. Chem.* 40:1219-1229).

One method of combinatorial chemistry, affinity fingerprinting, has previously been used to test a discrete library of small molecules for binding affinities for a defined panel of proteins. The fingerprints obtained by the screen are used to predict the affinity of the individual library members for other proteins or receptors of interest (in the instant invention, the protein complexes of the present invention and protein components thereof.) The fingerprints are compared with fingerprints obtained from other compounds known to react with the protein of interest to predict whether the library compound might similarly react. For example, rather than testing every ligand in a large library for interaction with a complex or protein component, only those ligands having a fingerprint similar to other compounds known to have that activity could be tested. (See, e.g., Kauvar et al., 1995, *Chem. Biol.* 2:107-118; Kauvar, 1995, *Affinity fingerprinting*, Pharmaceutical Manufacturing International. 8:25-28; and Kauvar, *Toxic-Chemical Detection by Pattern Recognition in New Frontiers in Agrochemical Immunoassay*, Kurtz, Stanker and Skeritt (eds), 1995, AOAC: Washington, D.C., 305-312).

Kay et al. (1993, *Gene* 128:59-65) disclosed a method of constructing peptide libraries that encode peptides of totally random sequence that are longer than those of any prior conventional libraries. The libraries disclosed in Kay et al. encode totally synthetic random peptides of greater than about 20 amino acids in length. Such libraries can be advantageously screened to identify complex modulators. (See also U.S. Patent No. 5,498,538 dated March 12, 1996; and PCT Publication No. WO 94/18318 dated August 18, 1994).

A comprehensive review of various types of peptide libraries can be found in Gallop et al., 1994, *J. Med. Chem.* 37:1233-1251.

PHARMACEUTICAL COMPOSITIONS AND THERAPEUTIC/PROPHYLACTIC ADMINISTRATION

The invention provides methods of treatment (and prophylaxis) by administration to a subject of an effective amount of a therapeutic of the invention. In a preferred aspect, the therapeutic is substantially purified. The subject is preferably an animal including, but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a

mammal, and most preferably human. In a specific embodiment, a non-human mammal is the subject.

Various delivery systems are known and can be used to administer a therapeutic of the invention, e.g., encapsulation in liposomes, microparticles, and microcapsules; use of recombinant cells capable of expressing the therapeutic, use of receptor-mediated endocytosis (e.g., Wu and Wu, 1987, *J. Biol. Chem.* 262:4429-4432); construction of a therapeutic nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds may be administered by any convenient route, for example by infusion, by bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral, rectal and intestinal mucosa, etc.), and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compositions of the invention locally to the area in need of treatment. This may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. In one embodiment, administration can be by direct injection at the site (or former site) of a malignant tumor or neoplastic or pre-neoplastic tissue.

In another embodiment, the therapeutic can be delivered in a vesicle, in particular a liposome (Langer, 1990, *Science* 249:1527-1533; Treat et al., 1989, In: *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler, eds., Liss, New York, pp. 353-365; Lopez-Berestein, *ibid.*, pp. 317-327; see generally *ibid.*)

In yet another embodiment, the therapeutic can be delivered via a controlled release system. In one embodiment, a pump may be used (Langer, *supra*; Sefton, 1987, *CRC Crit. Ref. Biomed. Eng.* 14:201-240; Buchwald et al., 1980, *Surgery* 88:507-516; Saudek et al., 1989, *N. Engl. J. Med.* 321:574-579). In another embodiment, polymeric materials can be

used (Medical Applications of Controlled Release, Langer and Wise, eds., CRC Press, Boca Raton, Florida, 1974; Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball, eds., Wiley, New York, 1984; Ranger and Peppas, 1983, *Macromol. Sci. Rev. Macromol. Chem.* 23:61; Levy et al., 1985, *Science* 228:190-192; During et al., 1989, *Ann. Neurol.* 25:351-356; Howard et al., 1989, *J. Neurosurg.* 71:858-863). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (e.g., Goodson, 1984, In: *Medical Applications of Controlled Release*, supra, Vol. 2, pp. 115-138). Other controlled release systems are discussed in the review by Langer (1990, *Science* 249:1527-1533).

In a specific embodiment where the therapeutic is a nucleic acid encoding a protein therapeutic, the nucleic acid can be administered in vivo to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by use of a retroviral vector (U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or by coating it with lipids, cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox-like peptide which is known to enter the nucleus (e.g., Joliot et al., 1991, *Proc. Natl. Acad. Sci. USA* 88:1864-1868), etc. Alternatively, a nucleic acid therapeutic can be introduced intracellularly and incorporated by homologous recombination within host cell DNA for expression.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a therapeutic, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly, in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, including but not limited to peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered orally. Saline and aqueous dextrose are preferred carriers when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions are preferably employed as liquid carriers for injectable solutions. Suitable pharmaceutical

excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsions, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the therapeutic, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated, in accordance with routine procedures, as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lidocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water or saline for injection can be provided so that the ingredients may be mixed prior to administration.

The therapeutics of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free carboxyl groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., those formed with free amine groups such as those derived from isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc., and those derived from sodium, potassium, ammonium, calcium, and ferric hydroxides, etc.

The amount of the therapeutic of the invention which will be effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. However, suitable dosage ranges for intravenous administration are generally about 20-500 micrograms of active compound per kilogram body weight. Suitable dosage ranges for intranasal administration are generally about 0.01 pg/kg body weight to 1 mg/kg body weight. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

Suppositories generally contain active ingredient in the range of 0.5% to 10% by weight; oral formulations preferably contain 10% to 95% active ingredient.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. For example, the kit can comprise in one or more containers a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group consisting of proteins listed in the third column of table 1; and a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins listed in the fourth column of table 1.

Alternatively, the kit can comprise in one or more containers, all proteins, functionally active fragments or functionally active derivatives thereof of from the group of proteins in the fifth column of table 1.

The kits of the present invention can also contain expression vectors encoding the essential components of the complex machinery, which components after being expressed can be reconstituted in order to form a biologically active complex. Such a kit preferably also

contains the required buffers and reagents. Optionally associated with such container(s) can be instructions for use of the kit and/or a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

ANIMAL MODELS

The present invention also provides animal models. In one embodiment, animal models for diseases and disorders involving the protein complexes of the present invention are provided. These animal models are well known in the art. These animal models include, but are not limited to those which are listed in the section "Screening for modulators of the protein complexes/proteins of the invention" (supra) as exemplary animal models to study any of the complexes provided in the invention. Such animals can be initially produced by promoting homologous recombination or insertional mutagenesis between genes encoding the protein components of the complexes in the chromosome, and exogenous genes encoding the protein components of the complexes that have been rendered biologically inactive or deleted (preferably by insertion of a heterologous sequence, e.g., an antibiotic resistance gene). In a preferred aspect, homologous recombination is carried out by transforming embryo-derived stem (ES) cells with one or more vectors containing one or more insertionally inactivated genes, such that homologous recombination occurs, followed by injecting the transformed ES cells into a blastocyst, and implanting the blastocyst into a foster mother, followed by the birth of the chimeric animal ("knockout animal") in which a gene encoding a component protein from the third column of table 1, or a functionally active fragment or functionally active derivative thereof, and a gene encoding a component protein from the fourth column of table 1, or a functionally active fragment or functionally active derivative thereof, has been inactivated or deleted (Capecchi, 1989, Science 244:1288-1292).

In another preferred aspect, homologous recombination is carried out by transforming embryo-derived stem (ES) cells with one or more vectors containing one or more insertionally inactivated genes, such that homologous recombination occurs, followed by injecting the transformed ES cells into a blastocyst, and implanting the blastocyst into a foster mother, followed by the birth of the chimeric animal ("knockout animal") in which the genes of all component proteins from the group of proteins listed in the third column of table 1 or of all

proteins from the group of proteins listed in the forth column of table 1 have been inactivated or deleted.

The chimeric animal can be bred to produce additional knockout animals. Such animals can be mice, hamsters, sheep, pigs, cattle, etc., and are preferably non-human mammals. In a specific embodiment, a knockout mouse is produced.

Such knockout animals are expected to develop, or be predisposed to developing, diseases or disorders associated with mutations involving the protein complexes of the present invention, and thus, can have use as animal models of such diseases and disorders, e.g., to screen for or test molecules (e.g., potential therapeutics) for such diseases and disorders.

In a different embodiment of the invention, transgenic animals that have incorporated and express (or over-express or mis-express) a functional gene encoding a protein component of the complex, e.g. by introducing the a gene encoding one or more of the components of the complex under the control of a heterologous promoter (i.e., a promoter that is not the native promoter of the gene) that either over-expresses the protein or proteins, or expresses them in tissues not normally expressing the complexes or proteins, can have use as animal models of diseases and disorders characterized by elevated levels of the protein complexes. Such animals can be used to screen or test molecules for the ability to treat or prevent the diseases and disorders cited supra.

In one embodiment, the present invention provides a recombinant non-human animal in which an endogenous gene encoding a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the group of proteins listed in the third column of table 1, and an endogenous gene encoding a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins listed in the fourth column of table 1 has been deleted or inactivated by homologous recombination or insertional mutagenesis of said animal or an ancestor thereof. In addition, the present invention provides a recombinant non-human animal in which the endogenous genes of all proteins, or functionally active fragments or functionally active derivatives thereof of one of the group of proteins listed in the fifth column have been deleted or inactivated by homologous recombination or insertional mutagenesis of said animal or an ancestor thereof:

In another embodiment, the present invention provides a recombinant non-human animal in which an endogenous gene encoding a first protein, or a functionally active fragment or functionally active derivative thereof, which first protein is selected from the

group consisting of proteins of the third column of table 1, and endogenous gene encoding a second protein, or a functionally active fragment or functionally active derivative thereof, which second protein is selected from the group consisting of proteins of the fourth column, of table 1 are recombinantly expressed in said animal or an ancestor thereof.

The invention further relates the following embodiments, to which the definitions, explanations and indications as given above also apply:

Embodiments relating to the Nicastrin complex (a):

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (ii) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
 - (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
 - (iv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
 - (v) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and

- (vi) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and
- (b) at least one second protein, which second protein is selected from the group consisting of:
- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
 - (ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,
 - (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
 - (iv) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,
 - (v) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
 - (vi) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

- (vii) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,
- (viii) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,
- (ix) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (x) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xi) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xiii) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (xiv) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein

tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(xv) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xvi) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(xvii) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

(xviii) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,

(xix) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xx) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxi) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,

(xxii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a

variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxiii) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxiv) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxv) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxvi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxvii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxviii) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes

to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and
(xxx) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

2. The protein complex according to No. 1 wherein the first protein is the protein "Nicastrin" (SEQ ID No:9), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid under low stringency conditions.

3. The protein complex according to No. 1 comprising the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that

hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,

(vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of

"ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions,

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

- (xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,
- (xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,
- (xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,
- (xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,
- (xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
- (xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a

variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 29 of the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a

nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,

(vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a

nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

(xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,

(xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or

several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps:

expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Nicastrin complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Nicastrin complex selected from

(i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,
- (x) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,
- (xi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger

protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and

(xii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C , washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55°C , and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C .

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising:

(a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.
18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.
19. The kit according to No. 18 for processing a substrate of said complex.
20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.
21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.
23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:
- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
 - (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(vii) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(viii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

- (x) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,
- (xi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,
- (x) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,
- (xi) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger

protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or

(xii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, comprising the steps of:

- (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
- (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:

- (a) exposing said complex, or a cell or organism containing Nicastrin complex to one or more candidate molecules; and
- (b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions, and/or
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

- (vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or
- (xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or

- (xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a

nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions, and/or

(xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions, and/or

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.
37. The method of No. 35, wherein the activity of said complex is determined.
38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.
40. The method of No. 39, wherein said determining step comprises determining whether
- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or
 - (ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit " encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit " nucleic acid or its complement under low stringency conditions, and/or
 - (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or
 - (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or

- (v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions, and/or
- (ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or
- (x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or
- (xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or

- (xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that

hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions, and/or

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions, and/or

(xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a

variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions, and/or

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes

to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "BACE1" (SEQ ID No:68) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (vi) "BSCv protein" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "BSCv protein" encoded by a nucleic acid that hybridizes to the "BSCv protein" nucleic acid or its complement under low stringency conditions,
- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "CGI-13" encoded by a

nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(viii) "Casein kinase II beta chain " (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Casein kinase II beta chain " encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain " nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xii) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xiii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xiv) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "FLJ22390" encoded by a

nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xvi) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Hypothetical protein tyrosine phosphatase ensg00000149185 " encoded by a nucleic acid that hybridizes to the "Hypothetical protein tyrosine phosphatase ensg00000149185 " nucleic acid or its complement under low stringency conditions,

(xvii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xviii) "KIAA1181" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1181" encoded by a nucleic acid that hybridizes to the "KIAA1181" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA1533" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "KIAA1533" encoded by a nucleic acid that hybridizes to the "KIAA1533" nucleic acid or its complement under low stringency conditions,

(xx) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Mesenchymal stem cell protein DSCD75 " encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75 " nucleic acid or its complement under low stringency conditions,

(xxi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxiii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxiv) "PP1, regulatory subunit 15B " (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "PP1, regulatory subunit 15B " encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B " nucleic acid or its complement under low stringency conditions,

(xxv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxvi) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxvii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxix) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protein similar to stromal cell-derived factor 2 " encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2 " nucleic acid or its complement under low stringency conditions,

(xxx) "Protocadherin beta 8 " (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Protocadherin

beta 8 " encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8 " nucleic acid or its complement under low stringency conditions,

(xxxi) "REP8 protein " (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "REP8 protein " encoded by a nucleic acid that hybridizes to the "REP8 protein " nucleic acid or its complement under low stringency conditions,

(xxxii) "RING finger protein 5 " (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "RING finger protein 5 " encoded by a nucleic acid that hybridizes to the "RING finger protein 5 " nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2 " encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2 " nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Stromal cell-derived factor 2-like 1 " encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1 " nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or(xxxvi) "Voltage-dependent anion channel 1" (SEQ ID No:102) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of "Voltage-dependent anion channel 1" encoded by a nucleic acid that hybridizes to the "Voltage-dependent anion channel 1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

The present invention further relates to the following embodiments of the Nicastrin-complex (b):

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein selected from the group consisting of:
 - (i) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
 - (ii) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
 - (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
 - (iv) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,
 - (v) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and
 - (vi) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and
 - (b) at least one second protein, which second protein is selected from the group consisting of:
 - (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to

the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(v) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(vi) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(vii) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(viii) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

- (ix) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,
- (x) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (xi) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (xii) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xiii) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,
- (xiv) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,
- (xv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (xvi) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xvii) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xviii) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xix) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xx) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiii) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxiv) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

- (xxv) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxvi) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,
- (xxvii) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xxviii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,
- (xxix) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,
- (xxx) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,
- (xxxi) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,
- (xxxii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger

protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xxxv) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and

(xxxvii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer

consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein 'Nicastrin' (SEQ ID NO. 147), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Nicastrin' encoded by a nucleic acid that hybridizes to the 'Nicastrin' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

- (vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,
- (viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,
- (x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,
- (xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,
- (xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,

(xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

- (xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,
- (xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,
- (xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,
- (xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that

hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xlili) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the

"tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions,

and a protein complex selected from complex (II) and comprising the following proteins:

- (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (vi) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,
- (vii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic

acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(viii) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(ix) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(x) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

(xi) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

(xii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiii) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xiv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,

(xv) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a

nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xvi) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xvii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xviii) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xix) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xx) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiii) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxv) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvi) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxvii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxviii) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxix) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxx) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxi) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxv) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxvi) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xxxviii) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant

of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xxxix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xl) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xli) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 36 of the following proteins:

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a

variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic

acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

(xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,

(xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390"

encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin"

encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions,

(xliii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in

cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Nicastrin complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the Nicastrin complex selected from

(i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(vii) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(viii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xi) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1,

regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xiii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and

(xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or

functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.

18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.

19. The kit according to No. 18 for processing a substrate of said complex.

20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.

22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
- (iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,
- (iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,
- (v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,
- (vii) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095"

encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(viii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xi) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xiii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

(i) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(iv) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(v) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(vi) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

- (vii) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,
- (viii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (x) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,
- (xi) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,
- (xii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,
- (xiii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the

"tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, comprising the steps of

- (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
- (b) determining whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing Nicastrin complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic

acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions, and/or

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic

acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or (xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or (xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or (xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or (xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions, and/or (xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions, and/or

- (xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or
- (xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or
- (xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or
- (xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions, and/or
- (xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger

protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xlili) "tyrosine phosphatase ens00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ens00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ens00000149185" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions, and/or

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions, and/or

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic

acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions, and/or

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B" encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions, and/or

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic

acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of

"KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or (xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions, and/or (xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions, and/or (xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions, and/or (xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or (xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or (xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions, and/or (xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions, and/or

- (xxxix) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions, and/or
- (xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions, and/or
- (xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions, and/or
- (xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions, and/or
- (xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions, and/or
- (xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger

protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or

(xlili) "tyrosine phosphatase ensG00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensG00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensG00000149185" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins
(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "18 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to the "18 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,
(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "25 kDa microsomal signal peptidase subunit" encoded by a nucleic acid that hybridizes to

the "25 kDa microsomal signal peptidase subunit" nucleic acid or its complement under low stringency conditions,

(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ATP-binding cassette, sub-family A, member 3" encoded by a nucleic acid that hybridizes to the "ATP-binding cassette, sub-family A, member 3" nucleic acid or its complement under low stringency conditions,

(iv) "Aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Aph-1a" encoded by a nucleic acid that hybridizes to the "Aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BSCv protein (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "BSCv protein (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(vii) "CAMK4" (SEQ ID No:104) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CAMK4" encoded by a nucleic acid that hybridizes to the "CAMK4" nucleic acid or its complement under low stringency conditions,

(viii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(ix) "Casein kinase II beta chain" (SEQ ID No:74) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Casein kinase II beta chain" encoded by a nucleic acid that hybridizes to the "Casein kinase II beta chain" nucleic acid or its complement under low stringency conditions,

(x) "Cathepsin B" (SEQ ID No:75) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cathepsin B"

encoded by a nucleic acid that hybridizes to the "Cathepsin B" nucleic acid or its complement under low stringency conditions,

(xi) "DCTN1" (SEQ ID No:106) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DCTN1" encoded by a nucleic acid that hybridizes to the "DCTN1" nucleic acid or its complement under low stringency conditions,

(xii) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,

(xiii) "ENSG00000144840" (SEQ ID No:79) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ENSG00000144840" encoded by a nucleic acid that hybridizes to the "ENSG00000144840" nucleic acid or its complement under low stringency conditions,

(xiv) "FACL3" (SEQ ID No:108) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xv) "FACL4" (SEQ ID No:109) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL4" encoded by a nucleic acid that hybridizes to the "FACL4" nucleic acid or its complement under low stringency conditions,

(xvi) "FLJ13977" (SEQ ID No:81) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ13977" encoded by a nucleic acid that hybridizes to the "FLJ13977" nucleic acid or its complement under low stringency conditions,

(xvii) "FLJ20342" (SEQ ID No:56) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20342" encoded by a nucleic acid that hybridizes to the "FLJ20342" nucleic acid or its complement under low stringency conditions,

(xviii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481"

encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ22390" (SEQ ID No:84) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ22390" encoded by a nucleic acid that hybridizes to the "FLJ22390" nucleic acid or its complement under low stringency conditions,

(xx) "ICAM-2" (SEQ ID No:87) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ICAM-2" encoded by a nucleic acid that hybridizes to the "ICAM-2" nucleic acid or its complement under low stringency conditions,

(xxi) "KIAA0095" (SEQ ID No:110) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0095" encoded by a nucleic acid that hybridizes to the "KIAA0095" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0922" (SEQ ID No:111) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0922" encoded by a nucleic acid that hybridizes to the "KIAA0922" nucleic acid or its complement under low stringency conditions,

(xxiii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1181 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1181 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxiv) "KIAA1533 (FRAGMENT)" (SEQ ID No:89) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1533 (FRAGMENT)" encoded by a nucleic acid that hybridizes to the "KIAA1533 (FRAGMENT)" nucleic acid or its complement under low stringency conditions,

(xxv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Mesenchymal stem cell protein DSCD75" encoded by a nucleic acid that hybridizes to the "Mesenchymal stem cell protein DSCD75" nucleic acid or its complement under low stringency conditions,

(xxvi) "NICE-3" (SEQ ID No:58) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NICE-3" encoded by a nucleic

acid that hybridizes to the "NICE-3" nucleic acid or its complement under low stringency conditions,

(xxvii) "Neurotrypsin" (SEQ ID No:92) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxviii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xxix) "PAS domain containing serine/threonine kinase" (SEQ ID No:112) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PAS domain containing serine/threonine kinase" encoded by a nucleic acid that hybridizes to the "PAS domain containing serine/threonine kinase" nucleic acid or its complement under low stringency conditions,

(xxx) "PP1, regulatory subunit 15B" (SEQ ID No:93) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PP1, regulatory subunit 15B" encoded by a nucleic acid that hybridizes to the "PP1, regulatory subunit 15B" nucleic acid or its complement under low stringency conditions,

(xxxi) "Pen-2" (SEQ ID No:10) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Pen-2" encoded by a nucleic acid that hybridizes to the "Pen-2" nucleic acid or its complement under low stringency conditions,

(xxxii) "Presenilin-1" (SEQ ID No:14) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-1" encoded by a nucleic acid that hybridizes to the "Presenilin-1" nucleic acid or its complement under low stringency conditions,

(xxxiii) "Presenilin-2" (SEQ ID No:66) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Presenilin-2" encoded by a nucleic acid that hybridizes to the "Presenilin-2" nucleic acid or its complement under low stringency conditions,

(xxxiv) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant

of "Protein amplified in osteosarcoma (OS-9)" encoded by a nucleic acid that hybridizes to the "Protein amplified in osteosarcoma (OS-9)" nucleic acid or its complement under low stringency conditions,

(xxxv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protein similar to stromal cell-derived factor 2" encoded by a nucleic acid that hybridizes to the "Protein similar to stromal cell-derived factor 2" nucleic acid or its complement under low stringency conditions,

(xxxvi) "Protocadherin beta 8" (SEQ ID No:96) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Protocadherin beta 8" encoded by a nucleic acid that hybridizes to the "Protocadherin beta 8" nucleic acid or its complement under low stringency conditions,

(xxxvii) "REP8 protein" (SEQ ID No:97) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "REP8 protein" encoded by a nucleic acid that hybridizes to the "REP8 protein" nucleic acid or its complement under low stringency conditions,

(xxxviii) "RING finger protein 5" (SEQ ID No:98) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RING finger protein 5" encoded by a nucleic acid that hybridizes to the "RING finger protein 5" nucleic acid or its complement under low stringency conditions,

(xxxix) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Retinal short-chain dehydrogenase/reductase retSDR2" encoded by a nucleic acid that hybridizes to the "Retinal short-chain dehydrogenase/reductase retSDR2" nucleic acid or its complement under low stringency conditions,

(xl) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Stromal cell-derived factor 2-like 1" encoded by a nucleic acid that hybridizes to the "Stromal cell-derived factor 2-like 1" nucleic acid or its complement under low stringency conditions,

(xli) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the

"Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xlii) "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" (SEQ ID No:113) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" encoded by a nucleic acid that hybridizes to the "homolog of yeast golgi membrane protein yif1p (yip1p-interacting factor)" nucleic acid or its complement under low stringency conditions, and/or(xliii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "tyrosine phosphatase ensg00000149185" encoded by a nucleic acid that hybridizes to the "tyrosine phosphatase ensg00000149185" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

Furthermore, the present invention relates to the Nicastrin-complex (c)

1. A protein complex selected from complex (not defined) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,

- (iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,
- (vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,
- (viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,
- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,
- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions, and
- (b) at least one first protein selected from the group consisting of:
 - (i) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic

acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(iii) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,

(iv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,

(v) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(vi) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(vii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(viii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(ix) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic

acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(x) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xi) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xiv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xv) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic

acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xviii) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xix) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xx) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxi) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxiii) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxiv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxv) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1"

encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxvi) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxvii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein APP-C99 (SEQ ID No:120), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'APP-C99' encoded by a nucleic acid that hybridizes to the 'APP-C99' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

- (iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,
- (iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,
- (vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,
- (viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,
- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,
- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,

acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,

(xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481"

encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic

acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1"

encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-27 of the following proteins:

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

- (v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,
- (vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,
- (viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,
- (ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,
- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,
- (xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (xiii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic

acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xx) "TTM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TTM2C" encoded by a nucleic acid that hybridizes to the "TTM2C" nucleic acid or its complement under low stringency conditions,

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic

acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic

acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin"

encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.
13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).
14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).
15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.

16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.

17. The kit according to No. 16 for processing a substrate of said complex.

18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.

20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic

acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,

(vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,

(viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,

(ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,

(x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,

(xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,

(xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xxi) "TTPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TTPR1" encoded by a nucleic acid that hybridizes to the "TTPR1" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.,and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:(a) exposing said complex, or a cell or organism containing Nicastrin-complex to one or more candidate molecules; and
(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether (i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions, and/or

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic

acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions, and/or

(ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions, and/or

(x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions, and/or

(xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions, and/or

(xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or

(xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic

acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions, and/or

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363"

encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic

acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxxiiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxxix) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1"

encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined.

34 The method of No. 32 wherein the activity of said complex is determined.

35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.

37 The method of No. 36 wherein said determining step comprises determining whether

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions, and/or

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions, and/or

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic

acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions, and/or

(vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions, and/or

(viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions, and/or

(ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions, and/or

(x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions, and/or

(xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions, and/or

(xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or

(xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic

acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions, and/or

(xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363"

encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic

acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions, and/or

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1"

encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.

42. Complex of any of No. 1 - 8 and/or protein selected from the following proteins

(i) "APP-C99" (SEQ ID No:120) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP-C99" encoded by a

nucleic acid that hybridizes to the "APP-C99" nucleic acid or its complement under low stringency conditions,

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iii) "Psen1" (SEQ ID No:3) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen1" encoded by a nucleic acid that hybridizes to the "Psen1" nucleic acid or its complement under low stringency conditions,

(iv) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(v) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(vi) "CtnnA1" (SEQ ID No:47) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA1" encoded by a nucleic acid that hybridizes to the "CtnnA1" nucleic acid or its complement under low stringency conditions,

(vii) "CtnnA2" (SEQ ID No:48) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnA2" encoded by a nucleic acid that hybridizes to the "CtnnA2" nucleic acid or its complement under low stringency conditions,

(viii) "CtnnB1" (SEQ ID No:46) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnB1" encoded by a nucleic acid that hybridizes to the "CtnnB1" nucleic acid or its complement under low stringency conditions,

(ix) "CtnnD1" (SEQ ID No:49) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CtnnD1" encoded by a nucleic acid that hybridizes to the "CtnnD1" nucleic acid or its complement under low stringency conditions,

- (x) "JUP" (SEQ ID No:2) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "JUP" encoded by a nucleic acid that hybridizes to the "JUP" nucleic acid or its complement under low stringency conditions,
- (xi) "NCadh" (SEQ ID No:50) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NCadh" encoded by a nucleic acid that hybridizes to the "NCadh" nucleic acid or its complement under low stringency conditions,
- (xii) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (xiii) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (xiv) "CK2B" (SEQ ID No:59) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CK2B" encoded by a nucleic acid that hybridizes to the "CK2B" nucleic acid or its complement under low stringency conditions,
- (xv) "CLGN" (SEQ ID No:54) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CLGN" encoded by a nucleic acid that hybridizes to the "CLGN" nucleic acid or its complement under low stringency conditions,
- (xvi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (xvii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (xviii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xix) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xx) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xxi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xxii) "KIAA0363" (SEQ ID No:105) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0363" encoded by a nucleic acid that hybridizes to the "KIAA0363" nucleic acid or its complement under low stringency conditions,

(xxiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xxiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xxv) "PTP LOC114971" (SEQ ID No:60) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTP LOC114971" encoded by a nucleic acid that hybridizes to the "PTP LOC114971" nucleic acid or its complement under low stringency conditions,

(xxvi) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2"

encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxvii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xxviii) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xxix) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxx) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxxi) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxxiii) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxxiv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded

by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxxv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions,

(xxxvi) "visinin-like 1" (SEQ ID No:37) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "visinin-like 1" encoded by a nucleic acid that hybridizes to the "visinin-like 1" nucleic acid or its complement under low stringency conditions,

(xxxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

The invention further relates to the following embodiments of the Bace1-complex (a)

1. A protein complex selected from complex (I) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and

(ii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and

- (b) at least one second protein, which second protein is selected from the group consisting of:
- (i) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,
 - (ii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
 - (iii) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,
 - (iv) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,
 - (v) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,
 - (vi) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
 - (vii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
 - (viii) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic

acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,

(ix) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(x) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,

(xi) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xii) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(xiii) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,

(xiv) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,

(xv) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,

(xvi) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related

receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,

(xvii) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xviii) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and

(xix) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein Bace1 (SEQ ID NO. 129), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Bace1' encoded by a nucleic acid that hybridizes to the 'Bace1' under low stringency conditions.

3. The protein complex according to No. 1 selected from complex (I) and comprising the following proteins:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic

acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,

(v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,

(viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,

(ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic

acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,

(xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,

(xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,

(xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic

acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,

(xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,

(xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1 - 18 of the following proteins:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that

hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,

(v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions,

(vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,

(vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,

(viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,

(ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,

(x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic

acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,

(xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,

(xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,

(xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,

(xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,

(xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the

"Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions,

(xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in

cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).

9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.

10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the BACE1 complex obtainable by a process according to any of No. 9 - 11.

13. Protein of the BACE1 complex selected from

(i) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

(ii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,

(iii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a

nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,

(iv) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,

(v) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and

(vi) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1 % SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

14. Nucleic acid encoding a protein according to No. 13.

15. Construct, preferably a vector construct, comprising (a) a nucleic acid according to No. 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or

(b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

16. Host cell, containing a vector comprising at least one of the nucleic acid of No. 14 and/or a construct of No. 15 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and an antibody or a fragment of said antibody which binds to any of the proteins according to No. 13.
18. A kit comprising in one or more container the complex of any of No. 1 - 8 and/or the proteins of No. 13 optionally together with an antibody according to No. 17 and/or further components such as reagents and working instructions.
19. The kit according to No. 18 for processing a substrate of said complex.
20. The kit according to No. 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.
21. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one protein according to No. 14 and/or at least one antibody according to No. 17 is attached to a solid carrier.
22. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

23. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (ii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
- (iii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
- (iv) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (v) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and a pharmaceutical acceptable carrier.

24. A pharmaceutical composition according to No. 23 for the treatment of diseases and disorders such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

25. A method for screening for a molecule that binds to the complex of anyone of No. 1 - 8 and/or any of the following the proteins:

- (i) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,
- (ii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
- (iii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
- (iv) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (v) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, comprising the steps of
 - (a) exposing said complex, or a cell or organism containing same to one or more candidate molecules; and
 - (b) determinig whether said candidate molecule is bound to the complex or protein.

26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of (a) exposing said complex, or a cell or organism containing BACE1 complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

27. The method of No. 26, wherein the amount of said complex is determined.

28. The method of No. 26, wherein the activity of said complex is determined.

29. The method of No. 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

30. The method of No. 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of No. 30, wherein said determining step comprises determining whether

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions, and/or
- (v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249". encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions, and/or

- (ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions, and/or
- (x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or

- (xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, is present in the complex.

32. The method of any of No. 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of No. 35, wherein the amount of said complex is determined.

37. The method of No. 35, wherein the activity of said complex is determined.

38. The method of No. 37, wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

39. The method of No. 35, wherein the amount of the individual protein components of said complex is determined.

40. The method of No. 39, wherein said determining step comprises determining whether

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions, and/or
- (v) "Delta-6 fatty acid desaturase " (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase " encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase " nucleic acid or its complement under low stringency conditions, and/or
- (vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions, and/or
- (viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions, and/or

- (ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions, and/or
- (x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions, and/or
- (xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions, and/or

(xix) "Thioredoxin domain-containing protein", (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions, and/or

(xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, is present in the complex.

41. The complex of any one of No. 1 - 8, or proteins of No. 13 or the antibody or fragment of No. 17, for use in a method of diagnosing a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the

amount of, the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

43. The method according to No. 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to No. 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

45. Complex of any of No. 1 - 8 and/or protein selected from the following proteins

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "CGI-13" (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13" encoded by a nucleic acid that hybridizes to the "CGI-13" nucleic acid or its complement under low stringency conditions,

(iii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Cadherin EGF LAG seven-pass G-type receptor 2" encoded by a nucleic acid that hybridizes to the "Cadherin EGF LAG seven-pass G-type receptor 2" nucleic acid or its complement under low stringency conditions,

- (iv) "Calsyntenin 1" (SEQ ID No:36) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Calsyntenin 1" encoded by a nucleic acid that hybridizes to the "Calsyntenin 1" nucleic acid or its complement under low stringency conditions,
- (v) "Delta-6 fatty acid desaturase" (SEQ ID No:76) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-6 fatty acid desaturase" encoded by a nucleic acid that hybridizes to the "Delta-6 fatty acid desaturase" nucleic acid or its complement under low stringency conditions,
- (vi) "Delta-like homolog" (SEQ ID No:118) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Delta-like homolog" encoded by a nucleic acid that hybridizes to the "Delta-like homolog" nucleic acid or its complement under low stringency conditions,
- (vii) "FLJ30668" (SEQ ID No:69) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ30668" encoded by a nucleic acid that hybridizes to the "FLJ30668" nucleic acid or its complement under low stringency conditions,
- (viii) "FLJ39249" (SEQ ID No:71) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ39249" encoded by a nucleic acid that hybridizes to the "FLJ39249" nucleic acid or its complement under low stringency conditions,
- (ix) "ITCH" (SEQ ID No:73) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITCH" encoded by a nucleic acid that hybridizes to the "ITCH" nucleic acid or its complement under low stringency conditions,
- (x) "KIAA1250" (SEQ ID No:107) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA1250" encoded by a nucleic acid that hybridizes to the "KIAA1250" nucleic acid or its complement under low stringency conditions,
- (xi) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

- (xii) "Nogo-A" (SEQ ID No:77) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nogo-A" encoded by a nucleic acid that hybridizes to the "Nogo-A" nucleic acid or its complement under low stringency conditions,
- (xiii) "PDGFRB" (SEQ ID No:78) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,
- (xiv) "PTK7" (SEQ ID No:80) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (xv) "SERPINA1" (SEQ ID No:83) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SERPINA1" encoded by a nucleic acid that hybridizes to the "SERPINA1" nucleic acid or its complement under low stringency conditions,
- (xvi) "SIM TO Y71H10A. 2.P" (SEQ ID No:85) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SIM TO Y71H10A. 2.P" encoded by a nucleic acid that hybridizes to the "SIM TO Y71H10A. 2.P" nucleic acid or its complement under low stringency conditions,
- (xvii) "STX10" (SEQ ID No:65) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STX10" encoded by a nucleic acid that hybridizes to the "STX10" nucleic acid or its complement under low stringency conditions,
- (xviii) "Sortilin-related receptor" (SEQ ID No:52) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Sortilin-related receptor" encoded by a nucleic acid that hybridizes to the "Sortilin-related receptor" nucleic acid or its complement under low stringency conditions,
- (xix) "Thioredoxin domain-containing protein" (SEQ ID No:101) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Thioredoxin domain-containing protein" encoded by a nucleic acid that hybridizes to the "Thioredoxin domain-containing protein" nucleic acid or its complement under low stringency conditions,

(xx) "integral membrane transporter protein" (SEQ ID No:114) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "integral membrane transporter protein" encoded by a nucleic acid that hybridizes to the "integral membrane transporter protein" nucleic acid or its complement under low stringency conditions, and/or (xxi) "kinectin 1 (kinesin receptor)" (SEQ ID No:90) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "kinectin 1 (kinesin receptor)" encoded by a nucleic acid that hybridizes to the "kinectin 1 (kinesin receptor)" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative diseases such as Alzheimer's disease and related neurodegenerative disorders.

Furthermore, the present invention relates to the BACE1-complex (b)

1. A protein complex selected from complex (not defined) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and

(b) at least one first protein selected from the group consisting of:

(i) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

- (ii) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,
- (v) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (vi) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (vii) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (viii) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (ix) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (x) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic

acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xi) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xii) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,

(xiii) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,

(xiv) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xv) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

(xvi) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,

(xvii) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xviii) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic

acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,

(xix) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xx) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxi) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiii) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxiv) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein BACE1 (SEQ ID No:38), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'BACE1' encoded by a nucleic acid that hybridizes to the 'BACE1' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (vii) "calsyntenin 1" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1"

encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,

(viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

(ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

(xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,

(xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,

(xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

(xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,

(xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-24 of the following proteins:

(i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions.

acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,

(v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

(vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,

(vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,

(viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

(ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

(xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,

(xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,

(xvi) "LAPTM4B" (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B" encoded by a nucleic acid that hybridizes to the "LAPTM4B" nucleic acid or its complement under low stringency conditions,

(xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

(xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,

(xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.
13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).
14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).
15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.
16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.
17. The kit according to No. 16 for processing a substrate of said complex.
18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.
19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.

20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,
- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (vii) "calsyntenin 1" (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1" encoded by a nucleic acid that hybridizes to the "calsyntenin 1" nucleic acid or its complement under low stringency conditions,

- (viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,

(xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,

(xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

(xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,

(xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions.,and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:(a) exposing said complex, or a cell or organism containing BACE1-complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the

complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or

- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions, and/or
- (viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or
- (ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or
- (x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or
- (xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or
- (xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

- (xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions, and/or
- (xiv) "TTM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TTM2C" encoded by a nucleic acid that hybridizes to the "TTM2C" nucleic acid or its complement under low stringency conditions, and/or
- (xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions, and/or
- (xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions, and/or

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined:

34 The method of No. 32 wherein the activity of said complex is determined.

35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.

37 The method of No. 36 wherein said determining step comprises determining whether

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions, and/or
- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions, and/or
- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or
- (vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions, and/or

(viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or

(ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or

(x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or

(xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions, and/or

- (xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions, and/or
- (xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions, and/or
- (xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions, and/or
- (xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions, and/or
- (xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions, and/or
- (xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions, and/or
- (xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2" encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions, and/or
- (xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of

beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.

42 Complex of any of No. 1 - 8 and/or protein selected from the following proteins

- (i) "BACE1" (SEQ ID No:38) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BACE1" encoded by a nucleic acid that hybridizes to the "BACE1" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "ACAT1" (SEQ ID No:4) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ACAT1" encoded by a nucleic acid that hybridizes to the "ACAT1" nucleic acid or its complement under low stringency conditions,
- (v) "APLP2" (SEQ ID No:22) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APLP2" encoded by a nucleic acid that hybridizes to the "APLP2" nucleic acid or its complement under low stringency conditions,

- (vi) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (vii) "calsyntenin 1 " (SEQ ID No:6) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "calsyntenin 1 " encoded by a nucleic acid that hybridizes to the "calsyntenin 1 " nucleic acid or its complement under low stringency conditions,
- (viii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (ix) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (x) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (xi) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (xii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (xiii) "GPR49" (SEQ ID No:115) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "GPR49" encoded by a nucleic acid that hybridizes to the "GPR49" nucleic acid or its complement under low stringency conditions,
- (xiv) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic

acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(xv) "KiDins220" (SEQ ID No:17) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KiDins220" encoded by a nucleic acid that hybridizes to the "KiDins220" nucleic acid or its complement under low stringency conditions,

(xvi) "LAPTM4B " (SEQ ID No:33) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "LAPTM4B " encoded by a nucleic acid that hybridizes to the "LAPTM4B " nucleic acid or its complement under low stringency conditions,

(xvii) "Neurotrypsin" (SEQ ID No:19) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Neurotrypsin" encoded by a nucleic acid that hybridizes to the "Neurotrypsin" nucleic acid or its complement under low stringency conditions,

(xviii) "NogoA" (SEQ ID No:41) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NogoA" encoded by a nucleic acid that hybridizes to the "NogoA" nucleic acid or its complement under low stringency conditions,

(xix) "OS-9" (SEQ ID No:42) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "OS-9" encoded by a nucleic acid that hybridizes to the "OS-9" nucleic acid or its complement under low stringency conditions,

(xx) "PDGFRB" (SEQ ID No:43) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PDGFRB" encoded by a nucleic acid that hybridizes to the "PDGFRB" nucleic acid or its complement under low stringency conditions,

(xxi) "PTK7 " (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7 " encoded by a nucleic acid that hybridizes to the "PTK7 " nucleic acid or its complement under low stringency conditions,

(xxii) "RetSDR2" (SEQ ID No:21) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "RetSDR2"

encoded by a nucleic acid that hybridizes to the "RetSDR2" nucleic acid or its complement under low stringency conditions,

(xxiii) "S100alpha" (SEQ ID No:34) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "S100alpha" encoded by a nucleic acid that hybridizes to the "S100alpha" nucleic acid or its complement under low stringency conditions,

(xxiv) "SORL1" (SEQ ID No:25) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORL1" encoded by a nucleic acid that hybridizes to the "SORL1" nucleic acid or its complement under low stringency conditions,

(xxv) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxvi) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvii) "UGCGL1" (SEQ ID No:45) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "UGCGL1" encoded by a nucleic acid that hybridizes to the "UGCGL1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

Furthermore, the present invention relates to the Psen2-complex

1. A protein complex selected from complex (not defined) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,

- (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and
- (b) at least one first protein selected from the group consisting of:
 - (i) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
 - (ii) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
 - (iii) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
 - (iv) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
 - (v) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
 - (vi) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,

- (vii) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (viii) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (ix) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,
- (x) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,
- (xi) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,
- (xii) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,
- (xiii) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,
- (xiv) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

- (xv) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,
- (xvi) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,
- (xvii) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,
- (xviii) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,
- (xix) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,
- (xx) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,
- (xxi) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,
- (xxii) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxiii) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxiv) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxv) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein Psen2 (SEQ ID No:121), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'Psen2' encoded by a nucleic acid that hybridizes to the 'Psen2' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

(i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,

(ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic

acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

(vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,

(vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a

nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xi) "TTPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TTPR1" encoded by a nucleic acid that hybridizes to the "TTPR1" nucleic acid or its complement under low stringency conditions,

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic

acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic

acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-25 of the following proteins:

(i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,

(ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,

(iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,

(iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,

(v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,

- (vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,
- (x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,
- (xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.

12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.
13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).
14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).
15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.
16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.
17. The kit according to No. 16 for processing a substrate of said complex.
18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.
19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.

20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,
- (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic

acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,

(xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,

(xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic

acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA

desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions.,and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:(a) exposing said complex, or a cell or organism containing Psen2-complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on

the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether

- (i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic

acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or

(iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or

(v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions, and/or

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic

acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions, and/or

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic

acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin"

encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined.
- 34 The method of No. 32 wherein the activity of said complex is determined.
35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.
- 37 The method of No. 36 wherein said determining step comprises determining whether
- (i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions, and/or
 - (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions, and/or
 - (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions, and/or
 - (iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions, and/or
 - (v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic

acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions, and/or

(vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions, and/or

(vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions, and/or

(viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions, and/or

(x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions, and/or

(xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions, and/or

(xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions, and/or

(xiii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic

acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions, and/or

(xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions, and/or

(xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions, and/or

(xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions, and/or

(xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions, and/or

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions, and/or

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions, and/or

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions, and/or

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic

acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions, and/or

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions, and/or

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions, and/or

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions, and/or

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions, and/or

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions, and/or

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions, and/or

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.

40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.

42 Complex of any of No. 1 - 8 and/or protein selected from the following proteins

(i) "Psen2" (SEQ ID No:121) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Psen2" encoded by a nucleic acid that hybridizes to the "Psen2" nucleic acid or its complement under low stringency conditions,

- (ii) "aph-1a" (SEQ ID No:1) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "aph-1a" encoded by a nucleic acid that hybridizes to the "aph-1a" nucleic acid or its complement under low stringency conditions,
- (iii) "Nicastrin" (SEQ ID No:9) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nicastrin" encoded by a nucleic acid that hybridizes to the "Nicastrin" nucleic acid or its complement under low stringency conditions,
- (iv) "CGI-13 " (SEQ ID No:72) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CGI-13 " encoded by a nucleic acid that hybridizes to the "CGI-13 " nucleic acid or its complement under low stringency conditions,
- (v) "DSCD75" (SEQ ID No:8) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DSCD75" encoded by a nucleic acid that hybridizes to the "DSCD75" nucleic acid or its complement under low stringency conditions,
- (vi) "ECSIT" (SEQ ID No:55) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ECSIT" encoded by a nucleic acid that hybridizes to the "ECSIT" nucleic acid or its complement under low stringency conditions,
- (vii) "FACL3" (SEQ ID No:11) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FACL3" encoded by a nucleic acid that hybridizes to the "FACL3" nucleic acid or its complement under low stringency conditions,
- (viii) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (ix) "FLJ10579" (SEQ ID No:12) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ10579" encoded by a nucleic acid that hybridizes to the "FLJ10579" nucleic acid or its complement under low stringency conditions,

- (x) "FLJ20481" (SEQ ID No:82) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FLJ20481" encoded by a nucleic acid that hybridizes to the "FLJ20481" nucleic acid or its complement under low stringency conditions,
- (xi) "ITPR1" (SEQ ID No:16) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITPR1" encoded by a nucleic acid that hybridizes to the "ITPR1" nucleic acid or its complement under low stringency conditions,
- (xii) "KIAA0090" (SEQ ID No:57) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "KIAA0090" encoded by a nucleic acid that hybridizes to the "KIAA0090" nucleic acid or its complement under low stringency conditions,
- (xviii) "MDR1" (SEQ ID No:18) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "MDR1" encoded by a nucleic acid that hybridizes to the "MDR1" nucleic acid or its complement under low stringency conditions,
- (xiv) "NicAChRa3" (SEQ ID No:62) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "NicAChRa3" encoded by a nucleic acid that hybridizes to the "NicAChRa3" nucleic acid or its complement under low stringency conditions,
- (xv) "PLD3" (SEQ ID No:20) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PLD3" encoded by a nucleic acid that hybridizes to the "PLD3" nucleic acid or its complement under low stringency conditions,
- (xvi) "SFXN1" (SEQ ID No:24) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SFXN1" encoded by a nucleic acid that hybridizes to the "SFXN1" nucleic acid or its complement under low stringency conditions,
- (xvii) "SLC4A2" (SEQ ID No:63) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SLC4A2" encoded by a nucleic acid that hybridizes to the "SLC4A2" nucleic acid or its complement under low stringency conditions,

(xviii) "SORT1" (SEQ ID No:15) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SORT1" encoded by a nucleic acid that hybridizes to the "SORT1" nucleic acid or its complement under low stringency conditions,

(xix) "SPC18" (SEQ ID No:26) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC18" encoded by a nucleic acid that hybridizes to the "SPC18" nucleic acid or its complement under low stringency conditions,

(xx) "SPC22" (SEQ ID No:27) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC22" encoded by a nucleic acid that hybridizes to the "SPC22" nucleic acid or its complement under low stringency conditions,

(xxi) "SPC25" (SEQ ID No:28) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPC25" encoded by a nucleic acid that hybridizes to the "SPC25" nucleic acid or its complement under low stringency conditions,

(xxii) "SPTLC2" (SEQ ID No:117) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "SPTLC2" encoded by a nucleic acid that hybridizes to the "SPTLC2" nucleic acid or its complement under low stringency conditions,

(xxiii) "stearoyl-CoA desaturase" (SEQ ID No:29) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "stearoyl-CoA desaturase" encoded by a nucleic acid that hybridizes to the "stearoyl-CoA desaturase" nucleic acid or its complement under low stringency conditions,

(xxiv) "STT3" (SEQ ID No:61) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "STT3" encoded by a nucleic acid that hybridizes to the "STT3" nucleic acid or its complement under low stringency conditions,

(xxv) "TMP21" (SEQ ID No:30) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TMP21" encoded by a nucleic acid that hybridizes to the "TMP21" nucleic acid or its complement under low stringency conditions,

(xxvi) "VLCAD" (SEQ ID No:31) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "VLCAD" encoded by a nucleic acid that hybridizes to the "VLCAD" nucleic acid or its complement under low stringency conditions,

(xxvii) "Wolframin" (SEQ ID No:67) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Wolframin" encoded by a nucleic acid that hybridizes to the "Wolframin" nucleic acid or its complement under low stringency conditions,

(xxviii) "YME1L1" (SEQ ID No:32) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "YME1L1" encoded by a nucleic acid that hybridizes to the "YME1L1" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

Furthermore, the present invention relates to the PTK7-complex

1. A protein complex selected from complex (not defined) and comprising

(a) at least one first protein selected from the group consisting of:

(i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and

(b) at least one first protein selected from the group consisting of:

(i) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,

(ii) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic

acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

(iii) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

(iv) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,

(v) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,

(vi) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(vii) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,

(viii) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40 Celsius, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55 Celsius, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60 Celsius.

2. The protein complex according to No. 1 wherein the first protein is the protein PTK7 (SEQ ID No:44), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of 'PTK7' encoded by a nucleic acid that hybridizes to the 'PTK7' under low stringency conditions.

3. The protein complex according to No. 1 - 2 and comprising the following proteins:

- (i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,

(viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,

(ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions.

4. The protein complex according to No. 1 comprising all but 1-8 of the following proteins:

(i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,

(iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,

(iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,

(v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,

- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,
- (viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,
- (x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions.

5. The complex of any of No. 1 - 4 comprising a functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein, respectively.

6. The complex of No. 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.

7. The complex of any of No. 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.

8. The complex of any of No. 1 - 7 that is involved in the transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)).
9. A process for preparing a complex of any of No. 1 - 8 and optionally the components thereof comprising the following steps: expressing a protein (bait) of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the bait protein, and optionally dissociating the protein complex and isolating the individual complex members.
10. The process according to No. 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of No. 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of the Fe65 complex obtainable by a process according to any of No. 9 - 11.
13. Construct, preferably a vector construct, comprising at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative of at least one of said proteins, or functionally active fragments or functionally active derivative thereof being selected from the first group of proteins according to No. 1 (a) and at least one of said proteins, or functionally active fragments or

functionally active derivative thereof being selected from the second group of proteins according to No. 1 (b).

14. Host cell, containing a construct of No. 13 or containing several vectors each comprising at least the nucleic acid sequence encoding at least one of the proteins, or functionally active fragments or functionally active derivatives thereof selected from the first group of proteins according to No. 1 (a) and the proteins, or functionally active fragments or functionally active derivatives thereof selected from the second group of proteins according to No. 1 (b).

15. An antibody or a fragment of said antibody containing the binding domain thereof, selected from an antibody or fragment thereof, which binds the complex of any of No. 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed.

16. A kit comprising in one or more container the complex of any of No. 1 - 8 optionally together with an antibody according to No. 15 and/or further components such as reagents and working instructions.

17. The kit according to No. 16 for processing a substrate of said complex.

18. The kit according to No. 16 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

19. Array, in which at least a complex according to any of No. 1 - 8 and/or at least one antibody according to No. 15 is attached to a solid carrier.

20. A process for processing a physiological substrate of the complex comprising the step of bringing into contact a complex to any of No. 1 - 8 with said substrate, such that said substrate is processed.

21. A pharmaceutical composition comprising the protein complex of any of No. 1 - 8 and/or any of the following the proteins:

- (i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,
- (viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like "

encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions.,and a pharmaceutical acceptable carrier.

22. A pharmaceutical composition according to No. 21 for the treatment of diseases and disorders such as neurodegenerative disease such as Alzheimer's disease.

23. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of No. 1 - 8 comprising the steps of:(a) exposing said complex, or a cell or organism containing PTK7-complex to one or more candidate molecules; and

(b) determining the amount of activity of protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity or composition of said complex.

24. The method of No. 23, wherein the amount of said complex is determined.

25. The method of No. 23 wherein the activity of said complex is determined.

26. The method of No. 25 wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and

determining the processing of said substrate is modified in the presence of said candidate molecule.

27. The method of No. 24 wherein the amount of the individual protein components of said complex are determined.

28 The method of No. 27 wherein said determining step comprises determining whether (i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or

(ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or

(iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or

(iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or

(v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(vii) "HIFPH3/EGLN3" (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3"

encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions, and/or

(viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions, and/or

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, is present in the complex.

29. The method of any of No. 23- 28 wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

30. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of No. 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

31. A method for the production of a pharmaceutical composition comprising carrying out the method of any of No. 1 - 8 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.

32. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, activity of, or component composition of, or intracellular localization of the complex of any one of the No. 1 - 8, comprising determining

the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicates the presence in the subject of the disease or disorder or predisposition in the subject.

33. The method of No. 32 wherein the amount of said complex is determined.

34 The method of No. 32 wherein the activity of said complex is determined.

35. The method of No. 34 wherein said determining step comprises isolating from the subject said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

36. The method of No. 32 wherein the amount of the individual protein components of said complex is determined.

37 The method of No. 36 wherein said determining step comprises determining whether

- (i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions, and/or
- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions, and/or
- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that

hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions, and/or

(iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions, and/or

(v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions, and/or

(vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions, and/or

(vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions, and/or

(viii) "TTM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "TTM2C" encoded by a nucleic acid that hybridizes to the "TTM2C" nucleic acid or its complement under low stringency conditions, and/or

(ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions, and/or

(x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, is present in the complex.

38. The complex of any one of No. 1 - 8, or the antibody or fragment of No. 15, for use in a method of diagnosing a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.
39. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity or component composition of or intracellular localization of, the complex of anyone of No. 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, transactivation of a Gal4-driven reporter gene (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of Abeta-40 and Abeta-42 peptides by ELISA (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), the production of C-terminal APP fragments in cell lines or transgenic animals by western blot (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)) or the proteolytic activity of beta- or gamma secretases towards bacterially expressed APP fragments in vitro (e.g. by modifying the expression of one or several interacting proteins in cells by means of RNAi (siRNA) and/or plasmids encoding the interacting protein(s)), or protein components of, said complex.
40. The method according to No. 39 wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
41. The method according to No. 39 wherein said disease or disorder involves increased levels of the amount or activity of said complex.
- 42 Complex of any of No. 1 - 8 and/or protein selected from the following proteins
(i) "PTK7" (SEQ ID No:44) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "PTK7" encoded by a nucleic acid that hybridizes to the "PTK7" nucleic acid or its complement under low stringency conditions,

- (ii) "APP" (SEQ ID No:23) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "APP" encoded by a nucleic acid that hybridizes to the "APP" nucleic acid or its complement under low stringency conditions,
- (iii) "BRI" (SEQ ID No:5) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "BRI" encoded by a nucleic acid that hybridizes to the "BRI" nucleic acid or its complement under low stringency conditions,
- (iv) "CELSR2" (SEQ ID No:39) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "CELSR2" encoded by a nucleic acid that hybridizes to the "CELSR2" nucleic acid or its complement under low stringency conditions,
- (v) "DLK1" (SEQ ID No:7) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "DLK1" encoded by a nucleic acid that hybridizes to the "DLK1" nucleic acid or its complement under low stringency conditions,
- (vi) "FADS2" (SEQ ID No:40) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "FADS2" encoded by a nucleic acid that hybridizes to the "FADS2" nucleic acid or its complement under low stringency conditions,
- (vii) "HIFPH3/EGLN3 " (SEQ ID No:64) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "HIFPH3/EGLN3 " encoded by a nucleic acid that hybridizes to the "HIFPH3/EGLN3 " nucleic acid or its complement under low stringency conditions,
- (viii) "ITM2C" (SEQ ID No:13) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "ITM2C" encoded by a nucleic acid that hybridizes to the "ITM2C" nucleic acid or its complement under low stringency conditions,
- (ix) "Nap1-like " (SEQ ID No:116) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Nap1-like " encoded by a nucleic acid that hybridizes to the "Nap1-like " nucleic acid or its complement under low stringency conditions,
- (x) "Reelin" (SEQ ID No:51) or a functionally active derivative thereof, or a functionally active fragment thereof, or a homolog thereof, or a variant of "Reelin" encoded by a nucleic acid that hybridizes to the "Reelin" nucleic acid or its complement under low stringency conditions, as a target for an active agent of a pharmaceutical, preferably a drug target in the

treatment or prevention of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease.

The invention further relates to the following embodiments:

1. A protein complex selected from complex (I) and comprising
 - (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
 - (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of said complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;and a complex (II) comprising at least two of said second proteins, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
2. A protein complex comprising a first protein selected from the proteins listed in table 1, second column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of a given complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low

stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

3. A protein complex comprising the proteins selected from the proteins in table 1, third column or a homologue thereof, or a variant thereof or functionally active fragments or functionally active derivatives of said proteins, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions; wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or a homologue or a variant thereof, or a functionally active fragment or a functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, but 1 to the number of proteins listed in table 1, fifth column of said complex, or a homologue or a variant thereof, or a functionally active fragment or functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins of said fifth column under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

5. The complex of any of claims 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of claim 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of claims 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of claims 1 - 7 that is involved in the biochemical activity as stated in table 3.
9. A process for preparing a complex of any of claims 1 - 8 and optionally the components thereof comprising the following steps:
expressing a protein of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the protein, preferably a tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.
10. The process according to claim 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of claims 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of claims 9 - 11.

13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
14. Nucleic acid encoding a protein according to claim 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to claim 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to claim 1 (a) and at least one of said proteins, being selected from the second group of proteins according to claim 1 (b).
16. Host cell, containing a vector comprising at least one of the nucleic acid of claim 14 and/or a construct of claim 15 or containing several vectors each comprising at least the nucleic acid encoding at least one protein selected from the first group of proteins according to claim 1 (a) and the nucleic acid encoding at least one protein selected from the second group of proteins according to claim 1 (b).
17. An antibody or a fragment of said antibody containing the binding domain thereof, which binds the complex of any of claims 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and/or an antibody or a fragment of said antibody

containing the binding domain thereof which binds to any of the group of proteins according to claim 13.

18. A kit comprising in one or more containers the complex of any of claims 1 - 8 and/or the proteins of claim 13, optionally together with an antibody according to claim 17 and/or further components such as reagents and working instructions.
19. The kit according to claim 18 for processing a substrate of a complex of any one of claims 1 - 8.
20. The kit according to claim 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
21. Array in which at least a complex according to any of claims 1 - 8 and/or at least one protein according to claim 13 and/or at least one antibody according to claim 17 is attached to a solid carrier.
22. A process for processing a substrate of a complex of any one of claims 1 - 8 comprising the step of bringing into contact a complex to any of claims 1 - 8 with said substrate, such that said substrate is processed.
23. A pharmaceutical composition comprising the protein complex of any of claims 1 - 8 and/or any of the proteins according to claim 13.
24. A pharmaceutical composition according to claim 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
25. A method for screening for a molecule that binds to the complex of any one of claims 1 - 8 and/or any of the proteins of claim 13, comprising the following steps:
 - (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and

- (b) determining whether said candidate molecule is bound to the complex or protein.
26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of claims 1 - 8 comprising the steps of:
- (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.
27. The method of claim 26, wherein the amount of said complex is determined.
28. The method of claim 26, wherein the activity of said complex is determined.
29. The method of claim 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of claim 26, wherein the amount of the individual protein components of said complex are determined.

31. The method of claim 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of claims 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of claims 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
34. A method for the production of a pharmaceutical composition comprising carrying out the method of claims 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the claims 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the

disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.

36. The method of claim 35, wherein the amount of said complex is determined.
37. The method of claim 35, wherein the activity of said complex is determined.
38. The method of claim 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of claim 35, wherein the amount of the individual protein components of said complex are determined.
40. The method of claim 39, wherein said determining step comprises determining whether any of the proteins according to claim 13 is present in the complex.
41. The complex of any one of claims 1 - 8, or proteins of claim 13 or the antibody of fragment of claim 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of claims 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity or, or protein components of, said complex.
43. The method according to claim 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

44. The method according to claim 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of claims 1 - 8 and/or any of the proteins listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

And to the further embodiments:

1. A protein complex selected from the group consisting of
- A) complex (I), wherein complex (I) comprises
- (a) at least one first protein, which first protein is selected from the group of proteins in table 1, fourth column of a given complex, or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions; and
- (b) at least one second protein, which second protein is selected from the group of proteins in table 1, fifth column of the same complex as addressed in (a), or a functionally active derivative thereof, or a functionally active fragment thereof, or a homologue thereof, or a variant of said second protein encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions;
- and
- B) complex (II), which comprises at least two of said second proteins,
- wherein said low stringency conditions preferably comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer

consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

2. A protein complex comprising a first protein selected from the proteins listed in table 1, second column of a given complex or a homologue or variant thereof, or a functionally active fragment or functionally active derivative of said first protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said first protein under low stringency conditions, and at least one second protein selected from the group of proteins in table 1, fifth column of the same complex, or a variant or homologue thereof, or a functionally active fragment or a functionally active derivative of said second protein, the variant of said second protein being encoded by a nucleic acid that hybridizes to the nucleic acid of said second protein under low-stringency conditions, and wherein said low stringency conditions preferably comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4) 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
3. A protein complex comprising the proteins selected from the proteins in table 1, third column or a homologue thereof, or a variant thereof or functionally active fragments or functionally active derivatives of said proteins, said variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low stringency conditions; wherein said low stringency conditions preferably comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
4. A protein complex that comprises all proteins as listed in table 1, third column for a given complex or a homologue or a variant thereof, or a functionally active fragment or a

functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins under low stringency conditions, but 1 to the number of proteins listed in table 1, fifth column of said complex, or a homologue or a variant thereof, or a functionally active fragment or functionally active derivative thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of any of said proteins of said fifth column under low stringency conditions, wherein said low stringency conditions preferably comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1-5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.

5. The complex of any of claims 1 - 4 comprising at least one functionally active derivative of said first protein and/or a functionally active derivative of said second protein, wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an amino acid sequence different from the first protein or second protein.
6. The complex of claim 5 wherein the functionally active derivative is a fusion protein comprising said first protein or said second protein fused to an affinity tag or label.
7. The complex of any of claims 1 - 4 comprising a fragment of said first protein and/or a fragment of said second protein, which fragment binds to another protein component of said complex.
8. The complex of any of claims 1 - 7 that is involved in the biochemical activity as stated in table 3.
9. A process for preparing a complex of any of claims 1 - 8 and optionally the components thereof comprising the following steps:

expressing a protein of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the protein, preferably a tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.

10. The process according to claim 9 wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.
11. The process according to any of claims 9 - 10 wherein the two tags are separated by a cleavage site for a protease.
12. Component of a protein complex obtainable by a process according to any of claims 9 - 11.
13. Protein selected from the group of proteins in table 1, sixth column of a given complex or a homologue or a variant of thereof, or a functionally active fragment or a functionally active derivative of said protein, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid encoding said protein under low stringency conditions, wherein said low stringency conditions preferably comprise hybridization in a buffer comprising 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 ug/ml denatured salmon sperm DNA, and 10% (wt/vol) dextran sulfate for 18-20 hours at 40°C, washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 55°C, and washing in a buffer consisting of 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS for 1.5 hours at 60°C.
14. Nucleic acid encoding a protein according to claim 13.
15. Construct, preferably a vector construct, comprising
 - (a) a nucleic acid according to claim 14 and at least one further nucleic acid which is normally not associated with said nucleic acid, or
 - (b) at least two separate nucleic acid sequences each encoding a different protein, or a functionally active fragment or a functionally active derivative thereof, or a

- homologue or a variant thereof, at least one of said proteins being selected from the first group of proteins according to claim 1 (a) and at least one of said proteins, being selected from the second group of proteins according to claim 1 (b).
16. Host cell, containing a vector comprising at least one of the nucleic acid of claim 14 and /or a construct of claim 15 or containing several vectors each comprising at least the nucleic acid encoding at least one protein selected from the first group of proteins according to claim 1 (a) and the nucleic acid encoding at least one protein selected from the second group of proteins according to claim 1 (b).
 17. An antibody or a fragment of said antibody containing the binding domain thereof, which binds the complex of any of claims 1 - 8 and which does not bind any of the proteins of said complex when uncomplexed and/or an antibody or a fragment of said antibody containing the binding domain thereof which binds to any of the group of proteins according to claim 13.
 18. A kit comprising in one or more containers the complex of any of claims 1 - 8 and/or the proteins of claim 13, optionally together with an antibody according to claim 17 and/or further components such as reagents and working instructions.
 19. The kit according to claim 18 for processing a substrate of a complex of any one of claims 1 - 8.
 20. The kit according to claim 18 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
 21. Array in which at least a complex according to any of claims 1 - 8 and/or at least one protein according to claim 13 and/or at least one antibody according to claim 17 is attached to a solid carrier.

22. A process for processing a substrate of a complex of any one of claims 1 - 8 comprising the step of bringing into contact a complex to any of claims 1 - 8 with said substrate, such that said substrate is processed.
23. A pharmaceutical composition comprising the protein complex of any of claims 1 - 8 and/or any of the proteins according to claim 13.
24. A pharmaceutical composition according to claim 23 for the treatment of diseases and disorders, preferentially for diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
25. A method for screening for a molecule that binds to the complex of any one of claims 1 - 8 and/or any of the proteins of claim 13, comprising the following steps:
- (a) exposing said complex or protein, or a cell or organism containing said complex or said protein, to one or more candidate molecules; and
 - (b) determining whether said candidate molecule is bound to the complex or protein.
26. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of claims 1 - 8 comprising the steps of:
- (a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and
 - (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent upon the function of the complex and/or product of a gene dependent on the complex in the presence of the one or more candidate molecules, wherein a change in said amount, activity, protein components or intracellular localization relative to said amount, activity, protein components and/or intracellular localization and/or a change in the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in the

absence of said candidate molecules indicates that the molecule modulates function, activity, or composition of said complex.

27. The method of claim 26, wherein the amount of said complex is determined.
28. The method of claim 26, wherein the activity of said complex is determined.
29. The method of claim 28, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
30. The method of claim 26, wherein the amount of the individual protein components of said complex are determined.
31. The method of claim 30, wherein said determining step comprises determining whether any of the proteins listed in table 1, third column of said complex, or a functionally active fragment or a functionally active derivative thereof, or a variant or a homologue thereof, the variant being encoded by a nucleic acid that hybridizes to the nucleic acid of said protein under low-stringency conditions, is present in the complex.
32. The method of any of claims 26 - 31, wherein said method is a method of screening for a drug for treatment or prevention of a disease or disorder, preferentially of a disease or disorder selected from the diseases or disorders such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
33. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of claims 1 - 8 for the manufacture of a medicament for the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

34. A method for the production of a pharmaceutical composition comprising carrying out the method of claims 26 - 31 to identify a molecule that modulates the function, activity, composition or formation of said complex, and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
35. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of the claims 1 - 8, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex and/or the transcription level of a gene dependent on the complex and/or the abundance and/or activity of a protein or protein complex dependent on the function of the complex and/or product of a gene dependent on the complex in a comparative sample derived from a subject, wherein a difference in said amount, activity, or protein components of, said complex in an analogous sample from a subject not having the disease or disorder or predisposition indicated the presence in the subject of the disease or disorder or predisposition in the subject.
36. The method of claim 35, wherein the amount of said complex is determined.
37. The method of claim 35, wherein the activity of said complex is determined.
38. The method of claim 37, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
39. The method of claim 35, wherein the amount of the individual protein components of said complex are determined.

40. The method of claim 39, wherein said determining step comprises determining whether any of the proteins according to claim 13 is present in the complex.
41. The complex of any one of claims 1 - 8, or proteins of claim 13 or the antibody of fragment of claim 17, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
42. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of claims 1 - 8, comprising administering to a subject in need of such treatment or prevention a therapeutically effective amount of one or more molecules that modulate the amount of, activity or, or protein components of, said complex.
43. The method according to claim 42, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.
44. The method according to claim 42, wherein said disease or disorder involves increased levels of the amount or activity of said complex.
45. Complex of claims 1 - 8 and/or any of the proteins listed in table 1, fifth column of said complex as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

Tables and Figures

TABLES:

Table 1: Composition of Complexes

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Entry point'): Lists the bait proteins that have been chosen for the purification of the given complex.

Third column ('All interactors'): Lists all novel interactors which have been identified as members of the complex and all interactors which have been known to be associated with the bait so far.

Fourth column ('Known interactors'): Lists all interactors which have been known to be associated with the bait so far.

Fifth column ('Novel interactors of the complex'): Lists all novel interactors of the complex which have been identified in the experiments provided herein.

Sixth column: Separately lists the members of the newly identified complex which have not been annotated previously.

Table 2: Individual Proteins of the Complexes

First column ('Protein'): Lists in alphabetical order all proteins which have been identified as interactors of the complexes presented herein.

Second column ('SEQ ID'): Lists the SEQ ID (Sequence Identifications) of the proteins herein as used herein.

Third column ('IPI-Numbers'): Lists the IPI-Numbers of the proteins herein. The IPI-Numbers refer to the International Protein Index created by the European Bioinformatics Institute (EMBL-EBI), Hinxton, UK.

Fourth column ('Molecular Weight'): Lists the Molecular Weight of the proteins in Dalton.

Table 3: Biochemical Activities of the Complexes of the invention.

First column ('Name of complex'): Lists the name of the protein complexes as used herein.

Second column ('Biochemical Activity'): Lists biochemical activities of the complexes.

Assays in order to test these activities are also provided herein (infra).

FIGURES

Figure 1: Schematic representation of FADS2-containing protein complexes. FADS2 is a component of BACE1-, Nicastrin- and PTK7- protein complexes.

TAP-tagged BACE1, Nicastrin and PTK7 were retrovirally transduced into SKNBE2 neuroblastoma cells and the respective protein complexes were subsequently obtained by tandem-affinity purification. Associated proteins were identified by liquid chromatography-MS/MS.

Figure 2:

FADS2 is highly expressed in human brain.

FADS2-specific primers and equal amounts of total RNA from various human tissue sources were utilized for determination of relative expression levels of FADS2 by quantitative PCR. Three independent experiments were performed and all values were normalized to a human reference RNA (Universal Human Reference RNA, Stratagene, No. 740000).

Figure 3 A+B:

siRNA-mediated knock-down of FADS2 expression attenuates secretion of A β 1-42 from two different cell lines.

(upper panels) siRNAs directed against BACE1, FADS2 (A and B) or Luc3 were transfected into SKNBE2 neuroblastoma cells (FIGURE 3 A) or H4 neuroglioma cells (FIGURE 3 B) over-expressing mutant APP^{sw}. 48h after transfection growth medium was removed and cells were incubated over night in serum-free medium. Supernatants were collected and levels of A β 1-42 determined by ELISA (Innogenetics). At least three independent experiments were performed in duplicate.

(lower panels) siRNAs directed against FADS2 (A and B) or Luc3 were co-transfected with CTAP-FADS2 into SKNBE2 neuroblastoma cells (Figure 3 A) or H4 neuroglioma cells (Figure 3 B). 48h after transfection cells were lysed. 30 μ g of the lysates were separated by SDS-PAGE, transferred to nitrocellulose and probed with antibodies directed either against the TAP-tag or against tubulin.

Figure 4:

SCD4 is very highly expressed in human brain.

5 μ g of total RNA from various human tissue sources (Clontech) was reverse transcribed. Equal amounts of that cDNA and SCD4-specific primers were utilized for determination of relative expression levels of SCD4 by quantitative PCR. Three independent experiments were performed and all values were normalized to a human reference RNA (Stratagene).

Figure 5:

siRNA-mediated knock-down of SCD4 expression attenuates secretion of A β 1-42.

(left panel) siRNAs directed against BACE1, SCD4 or Luc3 were transfected into H4 neuroglioma cells over-expressing mutant APPsw. 48h after transfection growth medium was removed and cells were incubated over night in serum-free medium. Supernatants were collected and levels of A β 1-42 determined by ELISA (Innogenetics). At least three independent experiments were performed in duplicate.

(right panel) siRNA directed against SCD4 specifically reduces mRNA levels. Total RNA was prepared from H4/APPsw cells transfected with siRNA directed against either Luc3 or SCD4. After reverse transcription, relative amounts of SCD4 transcripts were determined by quantitative PCR. At least two independent experiments were performed.

Figure 6:

DEGS is highly expressed in human brain.

5 μ g of total RNA from various human tissue sources (Clontech) was reverse transcribed. Equal amounts of that cDNA and DEGS-specific primers were utilized for determination of relative expression levels of DEGS by quantitative PCR. Three independent experiments were performed and all values were normalized to a human reference RNA (Stratagene).

Figure 7:

siRNA-mediated knock-down of DEGS expression attenuates secretion of A β 1-42.

(left panel) siRNAs directed against BACE1, DEGS or Luc3 were transfected into H4 neuroglioma cells over-expressing mutant APPsw. 48h after transfection growth medium was removed and cells were incubated over night in serum-free medium. Supernatants were collected and levels of A β 1-42 determined by ELISA (Innogenetics). At least three independent experiments were performed in duplicate.

(right panel) siRNA directed against DEGS specifically reduces mRNA levels. Total RNA was prepared from H4/APPsw cells transfected with siRNA directed against either Luc3 or

DEGS. After reverse transcription, relative amounts of DEGS transcripts were determined by quantitative PCR. At least two independent experiments were performed.

EXAMPLES:

The following examples refer to all embodiments of the invention and especially to the embodiments as claimed in the claims.

The TAP-technology, which is more fully described in EP 1 105 508 B1 and in Rigaut, et al., 1999, Nature Biotechnol. 17:1030-1032 respectively was used and further adapted as described below for protein purification. Proteins were identified using mass spectrometry as described further below.

EXAMPLE 1: Construction of TAP-tagged bait

The cDNAs encoding the complete ORF were obtained by RT-PCR. Total RNA was prepared from appropriate cell lines using the RNeasy Mini Kit (Qiagen). Both cDNA synthesis and PCR were performed with the SUPERScript One-Step RT-PCR for Long templates Kit (Life Technologies) using gene-specific primers. After 35-40 cycles of amplification PCR-products with the expected size were gel-purified with the MinElute PCR Purification Kit (Qiagen) and, if necessary, used for further amplification. Low-abundant RNAs were amplified by nested PCR before gel-purification. Restriction sites for NotI were attached to PCR primers to allow subcloning of amplified cDNAs into the retroviral vectors pIE94-N/C-TAP thereby generating N- or C-terminal fusions with the TAP-tag (Rigaut et al., 1999, Nature Biotechnol. 17:1030-1032). N-terminal tagging was chosen for the following baits/entry points: Presenilin 1, Presenilin 2, Aph-1a, Aph-1b, Pen-2, APP, Tau, Fe65, Calsenilin. C-terminal tagging was chosen for the following baits/entry points: Nicastrin, Aph-1a, Aph-1b, BACE1 D215N, APP, APP695SW, APP-C99, Fe65, X11beta.

Clones were analyzed by restriction digest, DNA sequencing and by in vitro translation using the TNT T7 Quick Coupled Transcription/Translation System (Promega inc.). The presence of the proteins was proven by Western blotting using the protein A part of the TAP-tag for detection. Briefly, separation of proteins by standard SDS-PAGE was followed by semi-dry transfer onto a nitrocellulose membrane (PROTRAN, Schleicher&Schuell) using the MultiphorII blotting apparatus from Pharmacia Biotech. The transfer buffer consisted of 48 mM Tris, 39 mM glycine, 10% methanol and 0,0375% sodium dodecylsulfate. After blocking in phosphate-buffered saline (PBS) supplemented with 10%

dry milk powder and 0,1% Tween 20 transferred proteins were probed with the Peroxidase-Anti-Peroxidase Soluble Complex (Sigma) diluted in blocking solution. After intensive washing immunoreactive proteins were visualized by enhanced chemiluminescence (ECL; Amersham Pharmacia Biotech).

EXAMPLE 2: Preparation of Virus and infection

As a vector, a MoMLV-based recombinant virus was used.

The preparation has been carried out as follows:

1. Preparation of Virus

293 gp cells were grown to 100% confluency. They were split 1:5 on poly-L-Lysine plates (1:5 diluted poly-L-Lysine [0.01% stock solution, Sigma P-4832] in PBS, left on plates for at least 10 min.). On Day 2, 63 microgram of retroviral Vector DNA together with 13 microgram of DNA of plasmid encoding an appropriate envelope protein were transfected into 293 gp cells (Somia, et al., 1999, Proc. Natl. Acad. Sci. USA 96:12667-12672; Somia, et al. 2000, J. Virol. 74:4420-4424). On Day 3, the medium was replaced with 15 ml DMEM + 10% FBS per 15-cm dish. On Day 4, the medium containing viruses (supernatant) was harvested (at 24 h following medium change after transfection). When a second collection was planned, DMEM 10 % FBS was added to the plates and the plates were incubated for another 24 h. All collections were done as follows: The supernatant was filtered through 0.45 micrometer filter (Corning GmbH, cellulose acetate, 431155). The filter was placed into konical polyallomer centrifuge tubes (Beckman, 358126) that are placed in buckets of a SW 28 rotor (Beckman). The filtered supernatant was ultracentrifuged at 19400 rpm in the SW 28 rotor, for 2 hours at 21 degree Celsius. The supernatant was discarded. The pellet containing viruses was resuspended in a small volume (for example 300 microliter) of Hank's Balanced Salt Solution [Gibco BRL, 14025-092], by pipetting up and down 100-times, using an aerosol-safe tip. The viruses were used for transfection as described below.

2. Infection

Cells that were infected were plated one day before into one well of a 6-well plate. 4 hours before infection, the old medium on the cells was replaced with fresh medium. Only a minimal volume was added, so that the cells are completely covered (e.g. 700 microliter). During infection, the cells were actively dividing.

A description of the cells and their growth conditions is given further below ("3. Cell lines")

To the concentrated virus, polybrene (Hexadimethrine Bromide; Sigma, H 9268) was added to achieve a final concentration of 8 microgram/ml (this is equivalent to 2.4 microliter of the 1 milligram/ml polybrene stock per 300 microliter of concentrated retrovirus). The virus was incubated in polybrene at room temperature for 1 hour. For infection, the virus/polybrene mixture was added to the cells and incubated at 37 degree Celsius at the appropriate CO₂ concentration for several hours (e.g. over-day or over-night). Following infection, the medium on the infected cells was replaced with fresh medium. The cells were passaged as usual after they became confluent. The cells contain the retrovirus integrated into their chromosomes and stably express the gene of interest.

3. Cell lines

For expression, SKN-BE2 cells were used. SKN-BE2 cells (American Type Culture Collection-No. CRL-2271) were grown in 95% OptiMEM + 5% iron-supplemented calf serum.

The expression pattern of the TAP-tagged proteins was checked by immunoblot-analysis as described in Example 3, Nr. 3 and/or by immunofluorescence as described in Example 3, Nr. 1 or 2.

EXAMPLE 3: Checking of expression pattern of TAP-tagged proteins

The expression pattern of the TAP-tagged protein was checked by immunoblot analysis and/or by immunofluorescence. Immunofluorescence analysis was either carried out

according to No. 1 or to No. 2 depending on the type of the TAP-tagged protein. Immunoblot analysis was carried out according to No. 3.

1 Protocol for the indirect Immunofluorescence staining of fixed mammalian cells for plasma membrane and ER bound proteins

Cells were grown in FCS media on polylysine coated 8 well chamber slides to 50% confluency. Then fixation of the cells was performed in 4% ParaFormaldehyde diluted in Phosphate Buffer Saline (PBS) solution (0.14M Phosphate, 0.1M NaCl pH 7.4). The cells were incubated for 30 minutes at room temperature in 300 microliters per well. Quenching was performed in 0.1M Glycine in PBS for 2x 20 minutes at room temperature. Blocking was performed with 1% Bovine Serum Albumin (BSA) in 0.3% Saponin + PBS for at least 1 hour at room temperature. Incubation of the primary antibodies was performed in the blocking solution overnight at +4°C. The proper dilution of the antibodies was determined in a case to case basis. Cells were washed in PBS containing 0.3% Saponin for 2x 20 minutes at room temperature. Incubation of the secondary antibodies is performed in the blocking solution. Alexa 594 coupled goat anti-rabbit is diluted 1:1000 (Molecular Probes). Alexa 488 coupled goat anti-mouse is diluted 1:1000 (Molecular Probes). DAPI was used to label DNA. If Phalloidin was used to label F-actin, the drug is diluted 1:500 and incubated with the secondary antibodies. Cells were then washed again 2x 20 minutes at room temperature in PBS. The excess of buffer was removed and cells were mounted in a media containing an anti-bleaching agent (Vectashield, Vector Laboratories).

2 Protocol for the indirect Immunofluorescence staining of fixed mammalian cells for non-plasma membrane bound proteins:

Cells were grown in FCS media on Polylysine coated 8 well chamber slides to 50% confluency. Fixation of the cells was performed in 4% ParaFormaldehyde diluted in Phosphate Buffer Saline (PBS) solution (0.14M Phosphate, 0.1M NaCl pH 7.4) for 30 minutes at Room Temperature (RT), 300 microliters per well. Quenching was performed in 0.1M Glycine in PBS for 2x 20 minutes at room temperature. Permeabilization of cells was done with 0.5% Triton X-100 in PBS for 10 minutes at room temperature. Blocking was then done in 1% Bovine Serum Albumin (BSA) in 0.3% Saponin + PBS for at least 1 hour at RT

(Blocking solution). Incubation of the primary antibodies was performed in the blocking solution, overnight at +4°C. The proper dilution of the antibodies has to be determined in a case to case basis. Cells were washed in PBS containing 0.3% Saponin, for 2x 20 minutes at RT. Incubation of the secondary antibodies was performed in the blocking solution. Alexa 594 coupled goat anti-rabbit is diluted 1:1000 (Molecular Probes), Alexa 488 coupled goat anti-mouse is diluted 1:1000 (Molecular Probes). DAPI was used to label DNA. If Phalloidin is used to label F-actin, the drug is diluted 1:500 and incubated with the secondary antibodies. Cells were washed 2x 20 minutes at RT in PBS. The excess of buffer was removed and cells were mounted in a media containing an anti-bleaching agent (Vectashield, Vector Laboratories).

3 Immunoblot analysis

To analyze expression levels of TAP-tagged proteins, a cell pellet (from a 6-well dish) was lysed in 60 µl DNase I buffer (5% Glycerol, 100 mM NaCl, 0.8 % NP-40 (IGEPAL), 5 mM magnesium sulfate, 100 µg/ml DNase I (Roche Diagnostics), 50 mM Tris, pH 7.5, protease inhibitor cocktail) for 15 min on ice. Each sample was split into two aliquots. The first half was centrifuged at 13,000 rpm for 5 min. to yield the NP-40-extractable material in the supernatant; the second half (total material) was carefully triturated. 50 µg each of the NP-40-extractable material and the total material are mixed with DTT-containing sample buffer for 30 min at 50°C on a shaker and separated by SDS polyacrylamide gel electrophoresis on a precast 4-12% Bis-Tris gel (Invitrogen). Proteins were then transferred to nitrocellulose using a semi-dry procedure with a discontinuous buffer system. Briefly, gel and nitrocellulose membrane were stacked between filter papers soaked in either anode buffer (three layers buffer A1 (0.3 M Tris-HCl) and three layers buffer A2 (0.03 M Tris-HCl)) or cathode buffer (three layers of 0.03 M Tris-HCl, pH 9.4, 0.1 % SDS, 40 mM □-aminocaproic acid). Electrotransfer of two gels at once was performed at 600 mA for 25 min. Transferred proteins were visualized with Ponceau S solution for one min to control transfer efficiency and then destained in water. The membrane was blocked in 5% non-fat milk powder in TBST (TBS containing 0.05% Tween-20) for 30 min at room temperature. It was subsequently incubated with HRP-coupled PAP antibody (1:5000 diluted in 5% milk/TBST) for 1 h at room temperature, washed three times for 10 min in TBST. The blot membrane was finally soaked

in chemiluminescent substrate (ECL, Roche Diagnostics) for 2 min. and either exposed to X-ray film or analyzed on an imaging station.

EXAMPLE 4 Purification of protein complexes

Protein complex purification was adapted to the sub-cellular localization of the TAP-tagged protein and was performed as described below.

1 Lysate preparation for cytoplasmic proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of CZ lysis buffer (50 mM Tris-Cl, pH 7.4; 5 % Glycerol; 0,2 % IGEPAL; 1.5 mM $MgCl_2$; 100 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was incubated for 30 min on ice and spun for 10 min at 20,000g. The supernatant was subjected to an additional ultracentrifugation step for 1 h at 100,000g. The supernatant was recovered and rapidly frozen in liquid nitrogen or immediately processed further.

2 Lysate preparation for membrane proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of Membrane-Lysis buffer (50 mM Tris, pH 7.4; 7.5 % Glycerol; 1 mM EDTA; 150 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was spun for 10 min at 750g, the supernatant was recovered and subjected to an ultracentrifugation step for 1 h at 100,000g. The membrane pellet was resuspended in 7,5 ml of Membrane-Lysis buffer containing 0.8%

n-Dodecyl- β -D-maltoside and incubated for 1 h at 4°C with constant agitation. The sample was subjected to another ultracentrifugation step for 1h at 100,000g and the solubilized material was quickly frozen in liquid nitrogen or immediately processed further.

3 Lysate preparation for nuclear proteins

About 1×10^9 adherent cells (average) were harvested with a cell scraper and washed 3 times in ice-cold PBS (3 min, 550g). Collected cells were frozen in liquid nitrogen or immediately processed further. For cell lysis, the cell pellet was resuspended in 10 ml of Hypotonic-Lysis buffer (10 mM Tris, pH 7.4; 1.5 mM $MgCl_2$; 10 mM KCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and homogenized by 10 strokes of a tight-fitted pestle in a dounce homogenizer. The lysate was spun for 10 min at 2,000g and the resulting supernatant (S1) saved on ice. The nuclear pellet (P1) was resuspended in 5 ml Nuclear-Lysis buffer (50 mM Tris, pH 7.4; 1.5 mM $MgCl_2$; 20 % Glycerol; 420 mM NaCl; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT; containing 1 tablet of EDTA-free Protease inhibitor cocktail (Complete™, Roche) per 25 ml of buffer) and incubated for 30 min on ice. The sample was combined with S1, further diluted with 7 ml of Dilution buffer (110 mM Tris, pH 7.4; 0.7 % NP40; 1.5 mM $MgCl_2$; 25 mM NaF; 1 mM Na_3VO_4 ; 1 mM DTT), incubated on ice for 10 min and centrifuged at 100,000g for 1h. The final supernatant (S2) was frozen quickly in liquid nitrogen.

4 Tandem Affinity Purification

The frozen lysate was quickly thawed in a 37°C water bath, and spun for 20 min at 100,000g. The supernatant was recovered and incubated with 0.2 ml of settled rabbit IgG-Agarose beads (Sigma) for 2 h with constant agitation at 4°C. Immobilized protein complexes were washed with 10 ml of CZ lysis buffer (containing 1 Complete™ tablet (Roche) per 50 ml of buffer) and further washed with 5 ml of TEV cleavage buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0.1 % IGEPAL; 0.5 mM EDTA; 1 mM DTT). Protein-complexes were eluted by incubation with 5 μ l of TEV protease (GibcoBRL, Cat.No. 10127-017) for 1 h at 16°C in 150 μ l TEV cleavage buffer. The eluate was recovered and combined with 0.2 ml settled Calmodulin affinity beads (Stratagene) in 0.2 ml CBP binding buffer (10 mM Tris, pH 7.4;

100 mM NaCl; 0,1 % IGEPAL; 2mM MgAc; 2mM Imidazole; 1mM DTT; 4 mM CaCl₂) followed by 1 h incubation at 4°C with constant agitation. Immobilized protein complexes were washed with 10 ml of CBP wash buffer (10 mM Tris, pH 7.4; 100 mM NaCl; 0,1 % IGEPAL; 1mM MgAc; 1mM Imidazole; 1mM DTT; 2 mM CaCl₂) and eluted by addition of 600 µl CBP elution buffer (10 mM Tris, pH 8.0; 5 mM EGTA) for 5 min at 37°C. The eluate was recovered in a siliconized tube and lyophilized. The remaining Calmodulin resin was boiled for 5 min in 50 µl 4x Laemmli sample buffer. The sample buffer was isolated, combined with the lyophilised fraction and loaded on a NuPAGE gradient gel (Invitrogen, 4-12%, 1.5 mm, 10 well).

EXAMPLE 5 Protein Identification by Mass Spectrometry

1 Protein digestion prior to mass spectrometric analysis

Gel-separated proteins were reduced, alkylated and digested in gel essentially following the procedure described by Shevchenko et al., 1996, Anal. Chem. 68:850-858. Briefly, gel-separated proteins were excised from the gel using a clean scalpel, reduced using 10 mM DTT (in 5mM ammonium bicarbonate, 54°C, 45 min) and subsequently alkylated with 55 mM iodoacetamid (in 5 mM ammonium bicarbonate) at room temperature in the dark (30 min). Reduced and alkylated proteins were digested in gel with porcine trypsin (Promega) at a protease concentration of 12.5 ng/µl in 5mM ammonium bicarbonate. Digestion was allowed to proceed for 4 hours at 37°C and the reaction was subsequently stopped using 5 µl 5% formic acid.

2 Sample preparation prior to analysis by mass spectrometry

Gel plugs were extracted twice with 20 µl 1% TFA and pooled with acidified digest supernatants. Samples were dried in a vacuum centrifuge and resuspended in 13 µl 1% TFA.

3. Mass spectrometric data acquisition

Peptide samples were injected into a nano LC system (CapLC, Waters or Ultimate, Dionex) which was directly coupled either to a quadrupole TOF (QTOF2, QTOF Ultima, QTOF Micro, Micromass or QSTAR Pulsar, Sciex) or ion trap (LCQ Deca XP) mass spectrometer. Peptides were separated on the LC system using a gradient of aqueous and organic solvents (see below). Solvent A was 5% acetonitrile in 0.5% formic acid and solvent B was 70% acetonitrile in 0.5% formic acid.

Time (min)	% solvent A	% solvent B
0	95	5
5.33	92	8
35	50	50
36	20	80
40	20	80
41	95	5
50	95	5

Peptides eluting off the LC system were partially sequenced within the mass spectrometer.

4. Protein identification

The peptide mass and fragmentation data generated in the LC-MS/MS experiments were used to query fasta formatted protein and nucleotide sequence databases maintained and updated regularly at the NCBI (for the NCBI nr, dbEST and the human and mouse genomes) and European Bioinformatics Institute (EBI, for the human, mouse, *D. melanogaster* and *C. elegans* proteome databases). Proteins were identified by correlating the measured peptide mass and fragmentation data with the same data computed from the entries in the database using the software tool Mascot (Matrix Science; Perkins et al., 1999, Electrophoresis 20:3551-3567). Search criteria varied depending on which mass spectrometer was used for the analysis.

EXAMPLE 6. siRNA-Inhibition of FADS2, DEGS, SCD4

FADS2, DEGS and SCD4 were separately inhibited by siRNA-expression. Results are depicted in figures 3, 5, 7.

A RNAi gene expression perturbation strategy was employed for functional validation of FADS2 as an effector of APP processing: Two different siRNAs directed against FADS2 as well as siRNAs directed against BACE1 or Luc3 into SKNBE2 were transfected into neuroblastoma or H4 neuroglioma cells

siRNAs for human FADS2 were synthesized by Dharmacon Research Inc.

The sequences used for FADS2 are:

GCUGAAAUACCUGCCCUAC and GCAUGGCAUUGAAUACCAG

Transfection of SK-N-BE2 cells was performed using LipofectAMINE 2000 (Invitrogen) following the manufacturer's instructions. Briefly, the cells were seeded at a density of 1.0×10^4 cells in a final volume of 85 μ l per 96-well 12-16 hrs prior to transfection. 25 nM of siRNAs were mixed with 8 μ l Opti-MEM buffer (Gibco) and 60 ng carrier DNA, and the mixture was incubated for 20 minutes at room temperature before addition to the cells. 16 and 48 hrs post-transfection medium was replaced with 100 μ l or 200 μ l growth medium with or without serum, respectively. 72 hrs post-transfection 100 μ l supernatants were harvested for A β 42 ELISA. The assay was performed following the manufacturer's instructions (Innogenetics).

Transfection of H4 cells was performed using RNAiFect (Qiagen) following the manufacturer's instructions. Briefly, the cells were seeded at a density of 1.0×10^4 cells in a final volume of 100 μ l per 96-well 12-16 hrs prior to transfection. 270 nM (0,375 μ g) of siRNAs were mixed with 25 μ l EC-R buffer and 2,3 μ l of RNAiFect and incubated for 15 minutes at room temperature before addition to the cells. During complex formation medium on cells was replaced with 75 μ l of fresh growth medium. 5 hrs post-transfection the cells were washed once with growth medium and 100 μ l were added for further cultivation. 48 hrs post-transfection medium was replaced with 200 μ l serum-free growth medium. 72 hrs post-transfection 100 μ l supernatants were harvested for A β 42 ELISA. The assay was performed following the manufacturer's instructions (Innogenetics).

Knockdown efficiency of selected siRNAs was assessed at the protein level by co-transfecting siRNAs and corresponding TAP-tagged cDNA expression vectors or by using cell lines stably

expressing the respective tagged protein of interest. 48 hrs post-transfection extracts were prepared, proteins separated by SDS-PAGE and transferred to nitrocellulose. Western blots were probed with antibodies directed against the tag and tubulin.

We noticed that like siRNAs directed against the known effector of APP processing, BACE1, those targeting FADS2 caused significant attenuation of A β 1-42 secretion, whereas the Luc3 siRNA had no effect.

Thus, we could show, that surprisingly, FADS2 plays a functional role in the processing of APP. It was shown that by inhibiting FADS2, the production of the A β 1-42 peptide could be reduced.

We confirmed that both FADS2 siRNAs did indeed interfere with expression of the desaturase by co-transfection of a FADS2-CTAP plasmid and FADS2 or Luc3 siRNAs into SKNBE2 and H4 cells. 48 h after transfection we determined expression levels of FADS2-CTAP by Western Blot analysis with anti-TAP antibodies.

EXAMPLE .7. Determination of FADS2-activity

a) . Rat liver microsomal assay

(Obukowicz MG, Raz A, Pyla PD, Rico JG, Wendling JM, Needleman P (1998a)

Identification and characterization of a novel delta6/delta5 fatty acid desaturase inhibitor as a potential anti-inflammatory agent. *Biochem. Pharmacol.* 1;55(7): 1045-58; Obukowicz MG, Welsch DJ, Salsgiver WJ, Martin-Berger CL, Chinn KS, Duffin KL, Raz A, Needleman P (1998b) Novel, selective delta6 or delta5 fatty acid desaturase inhibitors as antiinflammatory agents in mice. *J. Pharmacol. Exp. Ther.* 287(1):157-66)

Rat microsomal membranes are obtained by standard biochemical fractionation procedures. In a 48-well plate the following components are mixed: a) 150 μ l buffer/cofactors (250 mM sucrose, 150 mM KCl, 40 mM NaF, 1.3 mM ATP, 1 mg/ml MgCl₂ * 5 H₂O, 1.5 mM reduced glutathione, 60 μ M reduced CoA, 330 μ M nicotinamide, 670 μ g/ml NADH, 100 mM sodium phosphate, pH 7.4); b) 50 μ l rat liver micro-somes (~500 μ g total protein); c) 2.2 μ l test compound (DMSO stock; 1% final DMSO concentration); d) 20 μ l (0.05 μ Ci) ¹⁴C-Fatty Acid Substrates.

Preferred substrate for FADS2 is α -linolenic acid ($^{14}\text{C}18:3n-3$). [The assay allows for simultaneous measurement of FADS1 ($\Delta 5$ desaturase) and SCD-1 activity ($\Delta 9$ desaturase). The substrates for these enzymatic activities are $^{14}\text{C}20:3n-3$ and stearic acid ($^{14}\text{C}18:0$), respectively.]

Samples are incubated at 37°C for 1 hr, and then reactions are stopped and fatty acid ester linkages hydrolyzed by incubation with $200\mu\text{l}$ 2.5N KOH in methanol:water (4:1) for 4 h at 65°C . Free fatty acids are protonated with $280\mu\text{l}$ formic acid and extracted into organic phase ($700\mu\text{l}$ hexane). $200\mu\text{l}$ from hexane layer are analyzed on AgNO_3 -thin-layer chromatography (TLC) plates. Plates are dried over night and activity is quantified by phosphoimager. As an alternative to TLC analysis, separation of samples could be achieved by HPLC.

b) Cellular assay

A cell line expressing high levels of FADS2 (such as ABMC-7 mastocytoma cells) is utilized. Cells are adapted to grow in serum-free HL-1 medium containing FADS2 substrates (such as $10\mu\text{M}$ linoleic acid/ $15\mu\text{M}$ fatty acid-free BSA). To measure FADS2 activity 2×10^5 cells of are plated per 48-well and then incubated in medium containing $10\mu\text{M}$ of a suitable substrate (such as α -linolenic acid ($^{14}\text{C}18:3n-3$)). To terminate fatty acid metabolism, the cell layer is washed with PBS and $200\mu\text{l}$ 2.5N KOH in methanol:water (4:1) are added. Samples are further processed as described above.

c) High-throughput screening assays using fatty acid synthetic enzymes (s. WO-03/019146, p.27 ff.)

The assay utilizes position-specifically tritiated fatty acyl-CoA esters in a microsomal assay format (see above). The method detects the release of tritiated water and circumvents the requirement of TLC- or HPLC analysis of ^{14}C -labeled fatty acids. For screening of FADS2 inhibitors suitable substrates (1 mCi/ml stock) are ^3H [6,9,12-octadecadienoic acid] (CoA conjugate of linoleic acid) and/or ^3H [9,12,15-octadecatrienoic acid] (CoA α -linolenic acid). The label should be position-specific at C6/C7.

Briefly, the following components are mixed (total volume: $100\mu\text{l}$): $2\mu\text{l}$ unlabeled 1.5 mM fatty acyl CoA, $1\mu\text{l}$ tritiated fatty acyl CoA, $10\mu\text{l}$ 20 mM NADH, compounds from DMSO stock, $67\mu\text{l}$ 100 mM phosphate buffer, pH 7.2. $80\mu\text{l}$ of this mix are added to $20\mu\text{l}$ of

microsomes (~20 μ g total protein) and reaction is allowed to proceed for 5-30 min at RT. 10 μ l 6% perchloric acid are added to stop the reaction. To sediment unused tritiated substrate, samples are vortexed with 100 μ l charcoal suspension and centrifuged at 13,000rpm for 10min at 4°C. 400 μ l of supernatant is analyzed in a liquid scintillation counter.

TABLE 1

COMPONENTS OF COMPLEXES

Name of complex	Entry Point	All interactors of the complex	Known interactors of the complex	Novel interactors of the complex	Proteins of unknown function
Nicastrin complex (a)	Nicastrin	18 kDa microsomal signal peptidase subunit	Aph-1a	18 kDa microsomal signal peptidase subunit	ATP-binding cassette, sub-family A, member 3
		25 kDa microsomal signal peptidase subunit	BACE1	25 kDa microsomal signal peptidase subunit	CGI-13
		Aph-1a	Nicastrin	ATP-binding cassette, sub-family A, member 3	ENSG00000144840
		ATP-binding cassette, sub-family A member 3	Pen-2	BSCv protein	FLJ20342
		BACE1	Presenilin-1	Casein kinase II beta chain	FLJ20481

	BScv protein	Presenilin-2	Cathepsin B	FLJ22390
	Casein kinase II beta chain		CGI-13	Hypothetical protein tyrosine phosphatase ensg000000149185
	Cathepsin B		Delta-6 fatty acid desaturase	KIAA1181
	CGI-13		ENSG000000144840	KIAA1533
	Delta-6 fatty acid desaturase		FLJ13977	PP1, regulatory subunit 15B
	ENSG000000144840		FLJ20342	RING finger protein 5
	FLJ13977		FLJ20481	Thioredoxin domain-containing protein
	FLJ20342		FLJ22390	
	FLJ20481		Hypothetical protein tyrosine phosphatase ensg000000149185	
	FLJ22390		ICAM-2	

		Hypothetical protein tyrosine phosphatase ensg00000149185		KIAA1181	
		ICAM-2		KIAA1533	
		KIAA1181		Mesenchymal stem cell protein DSCD75	
		KIAA1533		Neurotrypsin	
		Mesenchymal stem cell protein DSCD75		NICE-3	
		Neurotrypsin		Protein amplified in osteosarcoma (OS-9)	
		Nicastrin		PP1, regulatory subunit 15B	
		NICE-3		Protein similar to stromal cell-derived factor 2	
		Pen-2		Protocadherin beta 8	
		Presenilin-1		REP8 protein	

		Presenilin-2		Retinal short-chain dehydrogenase/reductase retSDR2	
		Protein amplified in osteosarcoma (OS-9)		RING finger protein 5	
		PP1, regulatory subunit 15B		Stromal cell-derived factor 2-like 1	
		Protein similar to stromal cell-derived factor 2		Thioredoxin domain- containing protein	
		Protocadherin beta 8		Voltage-dependent anion channel 1	
		REP8 protein			
		Retinal short-chain dehydrogenase/reductase retSDR2			
		RING finger protein 5			
		Stromal cell-derived			

		factor 2-like 1				
		Thioredoxin domain-containing protein				
		Voltage-dependent anion channel 1				
Nicastrin-complex (b)	Nicastrin	18 kDa microsomal signal peptidase subunit			18 kDa microsomal signal peptidase subunit	
		25 kDa microsomal signal peptidase subunit			25 kDa microsomal signal peptidase subunit	
		Aph-1a	Aph-1a			
		ATP-binding cassette, sub-family A, member 3			ATP-binding cassette, sub-family A, member 3	ATP-binding cassette, sub-family A, member 3
		BACE1	BACE1			
		BSCv protein (FRAGMENT)			BSCv protein (FRAGMENT)	
		CAMK4			CAMK4	

	Casein kinase II beta chain		Casein kinase II beta chain	
	Cathepsin B		Cathepsin B	
	CGI-13		CGI-13	CGI-13
	DCTN1		DCTN1	
	Delta-6 fatty acid desaturase		Delta-6 fatty acid desaturase	
	ENSG000000144840		ENSG000000144840	ENSG000000144840
	FACL3		FACL3	
	FACL4		FACL4	
	FLJ13977		FLJ13977	
	FLJ20342		FLJ20342	FLJ20342
	FLJ20481		FLJ20481	FLJ20481
	FLJ22390		FLJ22390	FLJ22390
	homolog of yeast golgi membrane protein yif1p (yip1p-interacting		homolog of yeast golgi membrane protein yif1p (yip1p-interacting	

	factor)		factor)	
	ICAM-2		ICAM-2	
	KIAA0095		KIAA0095	KIAA0095
	KIAA0922		KIAA0922	KIAA0922
	KIAA1181 (FRAGMENT)		KIAA1181 (FRAGMENT)	KIAA1181 (FRAGMENT)
	KIAA1533 (FRAGMENT)		KIAA1533 (FRAGMENT)	KIAA1533 (FRAGMENT)
	Mesenchymal stem cell protein DSCD75		Mesenchymal stem cell protein DSCD75	
	Neurotrypsin		Neurotrypsin	
	Nicastrin	Nicastrin		
	NICE-3		NICE-3	
	PAS domain containing serine/threonine kinase		PAS domain containing serine/threonine kinase	
	Pen-2	Pen-2		
	PP1, regulatory subunit		PP1, regulatory subunit	PP1, regulatory

	15B		15B	subunit 15B
	Presenilin-1	Presenilin-1		
	Presenilin-2	Presenilin-2		
	Protein amplified in osteosarcoma (OS-9)		Protein amplified in osteosarcoma (OS-9)	
	Protein similar to stromal cell-derived factor 2		Protein similar to stromal cell-derived factor 2	
	Protocadherin beta 8		Protocadherin beta 8	
	REP8 protein		REP8 protein	
	Retinal short-chain dehydrogenase/reductase retSDR2		Retinal short-chain dehydrogenase/reductase retSDR2	
	RING finger protein 5		RING finger protein 5	RING finger protein 5
	Stromal cell-derived factor 2-like 1		Stromal cell-derived factor 2-like 1	

	Thioredoxin domain-containing protein		Thioredoxin domain-containing protein	Thioredoxin domain-containing protein
	tyrosine phosphatase ensg00000149185		tyrosine phosphatase ensg00000149185	tyrosine phosphatase ensg00000149185
Nicastrin-complex (c)	Nicastrin	Nicastrin		
	Psen1		Psen1	
	aph-1a		aph-1a	
	APP		APP	
	CtnnA1		CtnnA1	
	CtnnA2		CtnnA2	
	CtnnB1		CtnnB1	
	CtnnD1		CtnnD1	
	JUP		JUP	
	NCadh		NCadh	
	ACAT1		ACAT1	
	CGI-13		CGI-13	

	CK2B		CK2B	
	CLGN		CLGN	
	ECSIT		ECSIT	
	FACL3		FACL3	
	FADS2		FADS2	
	FLJ20481		FLJ20481	
	ITM2C		ITM2C	
	ITPR1		ITPR1	
	KIAA0363		KIAA0363	
	MDR1		MDR1	
	Neurotrypsin		Neurotrypsin	
	PTP LOC114971		PTP LOC114971	
	RetSDR2		RetSDR2	
	SFXN1		SFXN1	
	SPC18		SPC18	
	SPC22		SPC22	

	SPC25		SPC25	
	SPTLC2		SPTLC2	
	stearoyl-CoA desaturase		stearoyl-CoA desaturase	
	STT3		STT3	
	TMP21		TMP21	
	UGCGLI		UGCGLI	
	visinin-like 1		visinin-like 1	
	Wolframin		Wolframin	
	YME1L1		YME1L1	
BACE1 (new)-complex (a)	BACE1	BACE1	BACE1	
	Cadherin EGF LAG seven-pass G-type receptor 2	Cadherin EGF LAG seven-pass G-type receptor 2	Cadherin EGF LAG seven-pass G-type receptor 2	Cadherin EGF LAG seven-pass G-type receptor 2
	Calsynenin 1	Calsynenin 1	Calsynenin 1	Calsynenin 1

	CGI-13		CGI-13	
	Delta-6 fatty acid desaturase		Delta-6 fatty acid desaturase	
	Delta-like homolog		Delta-like homolog	
	FLJ30668		FLJ30668	FLJ30668
	FLJ39249		FLJ39249	FLJ39249
	integral membrane transporter protein		integral membrane transporter protein	
	ITCH		ITCH	
	KIAA1250		KIAA1250	KIAA1250
	kinectin 1 (kinesin receptor)		kinectin 1 (kinesin receptor)	
	Nicastrin	Nicastrin		
	Nogo-A		Nogo-A	
	PDGFRB		PDGFRB	
	PTK7		PTK7	

		SERPINA1		SERPINA1	
		SIM TO Y71H10A. 2.P.		SIM TO Y71H10A. 2.P.	SIM TO Y71H10A. 2.P.
		Sortilin-related receptor		Sortilin-related receptor	
		STX10		STX10	
		Thioredoxin domain-containing protein		Thioredoxin domain-containing protein	Thioredoxin domain-containing protein
BACE1-complex (b)	BACE1	APP	APP		
		Nicastrin		Nicastrin	
		ACAT1		ACAT1	
		APLP2		APLP2	
		BRI		BRI	
		calsyntenin 1		calsyntenin 1	
		CELSR2		CELSR2	
		CGI-13		CGI-13	

	DLK1		DLK1	
	DSCD75		DSCD75	
	FADS2		FADS2	
	GPR49		GPR49	
	ITM2C		ITM2C	
	KiDins220		KiDins220	
	LAPTM4B		LAPTM4B	
	Neurotrypsin		Neurotrypsin	
	NogoA		NogoA	
	OS-9		OS-9	
	PDGFRB		PDGFRB	
	PTK7		PTK7	
	RetSDR2		RetSDR2	
	S100alpha		S100alpha	
	SORL1		SORL1	
	stearoyl-CoA desaturase		stearoyl-CoA	

					desaturase	
		TMP21				
		UGCG1				
Psen2-complex	Psen2	aph-1a		aph-1a		
		Nicastrin			Nicastrin	
		Nicastrin			Nicastrin	
		CGI-13			CGI-13	
		DSCD75			DSCD75	
		ECSIT			ECSIT	
		FACL3			FACL3	
		FADS2			FADS2	
		FLJ10579			FLJ10579	
		FLJ20481			FLJ20481	
		ITPR1			ITPR1	
		KIAA0090			KIAA0090	

	MDR1		MDR1	
	NicAChRa3		NicAChRa3	
	PLD3		PLD3	
	SFXN1		SFXN1	
	SLC4A2		SLC4A2	
	SORT1		SORT1	
	SPC18		SPC18	
	SPC22		SPC22	
	SPC25		SPC25	
	SPTLC2		SPTLC2	
	stearoyl-CoA desaturase		stearoyl-CoA desaturase	
	STT3		STT3	
	TMP21		TMP21	
	VLCAD		VLCAD	
	Wolframin		Wolframin	

		YME1L1		YME1L1	
PTK7-complex	PTK7	APP	APP		
		BRI		BRI	
		CELSR2		CELSR2	
		DLK1		DLK1	
		FADS2		FADS2	
		HIFPH3/EGLN3		HIFPH3/EGLN3	
		ITM2C		ITM2C	
		Nap1-like		Nap1-like	
		Reelin		Reelin	

TABLE 2

INDIVIDUAL PROTEINS OF THE COMPLEXES

Aph-1a	1	IPI00059964.1	28996
JUP	2	IPI00028128.1	81498
Psen1	3	IPI00028077.1	52668
ACAT1	4	IPI00019898.3	64833
BRI	5	IPI00031821.1	30338
calsyntenin 1	6	IPI00218869.1	108670
DLK1	7	IPI00218210.1	32910
DSCD75	8	IPI00010292.1	23865
Nicastrin	9	IPI00021983.1	78411
Pen-2	10	IPI00020516.1	12029
FACL3	11	IPI00031397.1	80346
FLJ10579	12	IPI00018730.1	52118
ITM2C	13	IPI00016014.1	30224
Presenilin 1	14	IPI00026333.1	52163
Sortilin 1	15	IPI00016022.1	92100
ITPR1	16	IPI00216955.1	314758
KiDins220	17	IPI00033429.1	197211
MDR1	18	IPI00027481.1	141463
Neurotrypsin	19	IPI00011063.2	97067
PLD3	20	IPI00163951.2	49573
RetSDR2	21	IPI00008260.1	32964
APLP2	22	IPI00031030.1	86956
APP	23	IPI00006608.1	86943

SFXN1	24	IPI00009368.2	35619
SORL1	25	IPI00022608.1	248441
SPC18	26	IPI00104128.1	20625
SPC22	27	IPI00030262.2	20253
SPC25	28	IPI00220125.1	25692
stearoyl-CoA desaturase	29	IPI00013007.2	41523
TMP21	30	IPI00028055.1	24976
VLCAD	31	IPI00163655.1	68788
YME1L1	32	IPI00099529.1	79832
LAPTM4B	33	IPI00020093.1	31735
S100alpha	34	IPI00220412.1	10546
Cadherin EGF LAG seven-pass G-type receptor 2	35	IPI00015346.1	317453
Calsyntenin 1	36	IPI00007257.1	109793
visinin-like 1	37	IPI00216313.1	22142
BACE1	38	IPI00216211.1	48212
CELSR2	39	IPI00015346.1	317453
FADS2 (delta-6-desaturase)	40	IPI00183786.1	52259
NogoA	41	IPI00219209.1	106360
OS-9	42	IPI00218476.1	76295
PDGFRB	43	IPI00015902.2	124093
PTK7	44	IPI00219694.1	118392
UGCGL1	45	IPI00024466.1	177190
CtnnB1	46	IPI00017292.1	
CtnnA1	47	IPI00215948.1	102776
CtnnA2	48	IPI00030907.1	105282
CtnnD1	49	IPI00182469.2	107349
NCadh	50	IPI00015717.1	99851
Reelin	51	IPI00021018.1	388402

- 400 -

Sortilin-related receptor	52	IPI00022608.1	248441
18 kDa microsomal signal peptidase subunit	53	IPI00104128.1	20625
CLGN	54	IPI00183309.1	73577
ECSIT	55	IPI00106506.1	49148
FLJ20342	56	IPI00015713.1	65084
KIAA0090	57	IPI00160376.1	111759
NICE-3	58	IPI00032413.1	28779
CK2B	59	IPI00010865.1	24942
PTP LOC114971	60	IPI00174190.1	22844
STT3	61	IPI00102885.1	80530
NicAChRa3	62	IPI00007259.1	55637
SLC4A2	63	IPI00337431.3	137009
HIFPH3/EGLN3	64	IPI00004971.1	52259
STX10	65	IPI00012264.2	28114
Presenilin 2	66	IPI00028485.1	50140
Wolframin	67	IPI00008711.1	100306
BACE1	68	IPI00011518.1	55764
FLJ30668	69	IPI00043733.1	33338
BSCv protein	70	IPI00031131.1	46480
FLJ39249	71	IPI00167501.1	27459
CGI-13	72	IPI00008847.1	52917
ITCH	73	IPI00061780.1	102803
Casein kinase II beta chain	74	IPI00010865.1	24942
Cathepsin B	75	IPI00013478.1	37808
Delta-6 fatty acid desaturase (FADS2)	76	IPI00003544.1	52259

Nogo-A	77	IPI00021766.3	129931
PDGFRB	78	IPI00015902.1	123968
ENSG00000144840	79	IPI00102897.1	26308
PTK7	80	IPI00012719.1	118260
FLJ13977	81	IPI00025520.1	53482
FLJ20481	82	IPI00016418.1	47655
SERPINA1	83	IPI00032180.1	46737
FLJ22390	84	IPI00009343.1	17098
SIM TO Y71H10A. 2.P.	85	IPI00170775.1	68184
Hypothetical protein tyrosine phosphatase ensg00000149185	86	IPI00102935.1	22844
ICAM-2	87	IPI00009477.1	30653
KIAA1181	88	IPI00003635.1	36879
KIAA1533	89	IPI00001841.1	72964
kinectin 1 (kinesin receptor)	90	IPI00032968.1	156093
Mesenchymal stem cell protein DSCD75	91	IPI00010292.1	23865
Neurotrypsin	92	IPI00011063.1	97012
PP1, regulatory subunit 15B	93	IPI00045837.1	79125
Protein amplified in osteosarcoma (OS-9)	94	IPI00013268.1	75562
Protein similar to stromal cell-derived factor 2	95	IPI00034198.1	23026
Protocadherin beta 8	96	IPI00009033.1	87624
REP8 protein	97	IPI00010353.1	30541
RING finger protein 5	98	IPI00012608.1	19881

Retinal short-chain dehydrogenase/reductase retSDR2	99	IPI00008260.1	32964
Stromal cell-derived factor 2-like 1	100	IPI00106642.2	23511
Thioredoxin domain-containing protein	101	IPI00001028.1	32535
Voltage-dependent anion channel 1	102	IPI00010430.1	30641
ATP-binding cassette, sub-family A member 3	103	IPI00017800.1	191388
CAMK4	104	IPI00002921.1	51926
KIAA0363	105	IPI00004538.1	156999
DCTN1	106	IPI00011446.1	127404
KIAA1250	107	IPI00033429.1	197211
FACL3	108	IPI00031397.1	80346
FACL4	109	IPI00029737.1	79188
KIAA0095	110	IPI00005680.1	93488
KIAA0922	111	IPI00021671.1	138688
PAS domain containing serine/threonine kinase	112	IPI00141040.1	142859
homolog of yeast golgi membrane protein yif1p (yif1p-interacting factor)	113	IPI00063544.1	33834
Integral membrane transporter protein	114	IPI00020093.1	31735
GPR49	115	IPI00021131.1	99998
NAP-1 related protein/NAP-1-like protein	116	IPI00155244.1	44159
SPTLC2	117	IPI00005751.1	62924
Delta-like homolog	118	IPI00009191.1	41143

- 403 -

25 kDa microsomal signal peptidase subunit	119	IPI00014148.1	25003
APP-C99	120		11278
Psen2	121	IPI00028485.1	50140

TABLE 3

BIOCHEMICAL ACTIVITIES OF THE COMPLEXES

Name of Complex	Biochemical activity
Nicastrin-complex	Gamma-secretase activity and assembly (trafficking)
Bace1-complex	APP processing beta-secretase
Psen-2-complex	Gamma-secretase activity
PTK7-complex	Role in neuronal signal transduction; involved in neural development and structural plasticity of the CNS; modulator of BACE function.

- 405 -

The present invention is not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the
5 appended claims.

Various publications are cited herein, the disclosures of which are incorporated by reference in their entireties.

The invention further relates to the use of a FADS2 interacting molecule for the
10 modulation of beta secretase and/or gamma secretase activity in vitro. With respect to this use of the invention, all embodiments with respect to the FADS2 interacting molecule and to the modulation of beta secretase and/or gamma secretase activity as present above in the context of the use of a FADS2 interacting molecule for the preparation of a pharmaceutical composition for the treatment of neurodegenerative diseases also apply.

15

CLAIMS

1. Use of a FADS2 interacting molecule for the preparation of a pharmaceutical composition for the treatment of neurogenerative diseases.
2. The use of claim 1, wherein the FADS2-interacting molecule is a FADS2 inhibitor.
3. The use of claim 2, wherein the inhibitor is selected from the group consisting of antibodies, antisense oligonucleotides, siRNA, low molecular weight molecules (LMWs), binding peptides, aptamers, ribozymes.
4. The use of any of claims 1 to 3, wherein FADS2 is part of a protein complex comprising at least one further protein selected from the proteins in table 1, third column.
5. The use of any of claims 1 to 4, wherein the interacting molecule or inhibitor modulates the activity of gamma secretase and/or beta secretase.
6. The use of any of claims 1 to 5, wherein the neurodegenerative disease is Alzheimer's disease
7. A method for identifying a gamma secretase and/or a beta secretase modulator, comprising the following steps:
 - a. identifying of a FADS2-interacting molecule by determining whether a given test compound is a FADS2-interacting molecule,
 - b. determining whether the FADS2-interacting molecule of step a) is capable of modulating gamma secretase and/or beta secretase activity.

8. The method of claim 7, wherein in step a) the test compound is brought into contact with FADS2 and the interaction of FADS2 with the test compound is determined.
- 5 9. The method of claim 8, wherein the interaction of the test compound with FADS2 results in an inhibition of FADS2 activity.
- 10 10. The method of any of claims 7 to 9, wherein in step b) the ability of the gamma secretase and/or the beta secretase to cleave APP is measured.
11. A method for preparing a pharmaceutical composition for the treatment of neurodegenerative diseases, comprising the following steps:
- 15 a. identifying a gamma secretase and/or beta secretase modulator according to claims 7 to 11, and
- b. formulating the gamma secretase and/or beta secretase modulator to a pharmaceutical composition.
- 20 12. A protein complex comprising
- a) FADS2 and
- 25 b) either one or more proteins of the Nicastrin (a) complex, of the Nicastrin (b) complex, of the Nicastrin (c) complex, of the BACE1-complex (a), of the BACE1-complex (b), of the Psen2-complex or of the PTK7 complex.
- 30 13. The complex of claim 5, wherein the one or more proteins of the Nicastrin (a) complex are selected from the group consisting of

(i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53)

- (ii) "25 kDa microsomal signal peptidase subunit " (SEQ ID No:119)
- (iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103),
- (iv) "Aph-1a" (SEQ ID No:1),
- 5 (v) "BACE1" (SEQ ID No:68),
- (vi) "BSCv protein" (SEQ ID No:70),
- (vii) "CGI-13" (SEQ ID No:72)
- (viii) "Casein kinase II beta chain " (SEQ ID No:74),
- (ix) "Cathepsin B" (SEQ ID No:75),
- 10 (x) "ENSG00000144840" (SEQ ID No:79)
- (xi) "FLJ13977" (SEQ ID No:81),
- (xii) "FLJ20342" (SEQ ID No:56),
- (xiii) "FLJ20481" (SEQ ID No:82),
- (xiv) "FLJ22390" (SEQ ID No:84),
- 15 (xv) "Hypothetical protein tyrosine phosphatase ensg00000149185 " (SEQ ID No:86),
- (xvi) "ICAM-2" (SEQ ID No:87)
- (xvii) "KIAA1181" (SEQ ID No:88),
- (xiii) "KIAA1533" (SEQ ID No:89),
- 20 (xix) "Mesenchymal stem cell protein DSCD75 " (SEQ ID No:91)
- (xx) "NICE-3" (SEQ ID No:58),
- (xxi) "Neurotrypsin" (SEQ ID No:92),
- (xxii) "Nicastrin" (SEQ ID No:9),
- (xxiii) "PP1, regulatory subunit 15B " (SEQ ID No:93)
- 25 (xxiv) "Pen-2" (SEQ ID No:10)
- (xxv) "Presenilin-1" (SEQ ID No:14),
- (xxvi) "Presenilin-2" (SEQ ID No:66),
- (xxvii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94)
- (xxviii) "Protein similar to stromal cell-derived factor 2 " (SEQ ID No:95)
- 30 (xxix) "Protocadherin beta 8 " (SEQ ID No:96)
- (xxx) "REP8 protein " (SEQ ID No:97)
- (xxxi) "RING finger protein 5 " (SEQ ID No:98)

(xxxii) "Retinal short-chain dehydrogenase/reductase retSDR2 " (SEQ ID No:99)
(xxxiii) "Stromal cell-derived factor 2-like 1 " (SEQ ID No:100)
5 (xxxiv) "Thioredoxin domain-containing protein" (SEQ ID No:101), and
(xxxv) "Voltage-dependent anion channel 1" (SEQ ID No:102),

and wherein the one or more proteins of the Nicastrin (b) complex are selected
from the group consisting of of

- 10 (i) "18 kDa microsomal signal peptidase subunit" (SEQ ID No:53)
(ii) "25 kDa microsomal signal peptidase subunit" (SEQ ID No:119)
(iii) "ATP-binding cassette, sub-family A, member 3" (SEQ ID No:103)
(iv) "Aph-1a" (SEQ ID No:1)
15 (v) "BACE1" (SEQ ID No:38)
(vi) "BSCv protein (FRAGMENT)" (SEQ ID No:70)
(vii) "CAMK4" (SEQ ID No:104)
(viii) "CGI-13" (SEQ ID No:72)
(ix) "Casein kinase II beta chain" (SEQ ID No:74)
20 (x) "Cathepsin B" (SEQ ID No:75)
(xi) "DCTN1" (SEQ ID No:106)
(xii) "ENSG00000144840" (SEQ ID No:79)
(xiii) "FACL3" (SEQ ID No:108)
(xiv) "FACL4" (SEQ ID No:109)
25 (xv) "FLJ13977" (SEQ ID No:81)
(xvi) "FLJ20342" (SEQ ID No:56)
(xvii) "FLJ20481" (SEQ ID No:82)
(xiii) "FLJ22390" (SEQ ID No:84)
(xix) "ICAM-2" (SEQ ID No:87)
30 (xx) "KIAA0095" (SEQ ID No:110)
(xxi) "KIAA0922" (SEQ ID No:111)
(xxii) "KIAA1181 (FRAGMENT)" (SEQ ID No:88)
(xxiii) "KIAA1533 (FRAGMENT)" (SEQ ID No:89)

- (xxiv) "Mesenchymal stem cell protein DSCD75" (SEQ ID No:91)
(xxv) "NICE-3" (SEQ ID No:58)
5 (xxvi) "Neurotrypsin" (SEQ ID No:92)
(xxvii) "Nicastrin" (SEQ ID No:9)
(xxiii) "PAS domain containing serine/threonine kinase" (SEQ ID No:112)
(xxix) "PP1, regulatory subunit 15B" (SEQ ID No:93)
(xxx) "Pen-2" (SEQ ID No:10)
10 (xxxi) "Presenilin-1" (SEQ ID No:14)
(xxxii) "Presenilin-2" (SEQ ID No:66)
(xxxiii) "Protein amplified in osteosarcoma (OS-9)" (SEQ ID No:94)
(xxxiv) "Protein similar to stromal cell-derived factor 2" (SEQ ID No:95)
(xxxv) "Protocadherin beta 8" (SEQ ID No:96)
15 (xxxvi) "REP8 protein" (SEQ ID No:97)
(xxxvii) "RING finger protein 5" (SEQ ID No:98)
(xxxiii) "Retinal short-chain dehydrogenase/reductase retSDR2" (SEQ ID No:99)
(xxxix) "Stromal cell-derived factor 2-like 1" (SEQ ID No:100)
(xl) "Thioredoxin domain-containing protein" (SEQ ID No:101)
20 (xli) "homolog of yeast golgi membrane protein yiflp (yip1p-interacting factor)"
(SEQ ID No:113), and
(xlii) "tyrosine phosphatase ensg00000149185" (SEQ ID No:86),

and wherein the one or more proteins of the Nicastrin (c) complex are selected from
25 the group consisting of

(i) "APP-C99" (SEQ ID No:120)
(ii) "Nicastrin" (SEQ ID No:9)
(iii) "Psen1" (SEQ ID No:3)
30 (iv) "aph-1a" (SEQ ID No:1)
(v) "APP" (SEQ ID No:23)
(vi) "CtnnA1" (SEQ ID No:47)
(vii) "CtnnA2" (SEQ ID No:48)

- (viii) "CtnnB1" (SEQ ID No:46)
(ix) "CtnnD1" (SEQ ID No:49)
5 (x) "JUP" (SEQ ID No:2)
(xi) "NCadh" (SEQ ID No:50)
(xii) "ACAT1" (SEQ ID No:4)
(xiii) "CGI-13" (SEQ ID No:72)
(xiv) "CK2B" (SEQ ID No:59)
10 (xv) "CLGN" (SEQ ID No:54)
(xvi) "ECSIT" (SEQ ID No:55)
(xvii) "FACL3" (SEQ ID No:11)
(xiii) "FLJ20481" (SEQ ID No:82)
(xix) "ITM2C" (SEQ ID No:13)
15 (xx) "ITPR1" (SEQ ID No:16)
(xxi) "KIAA0363" (SEQ ID No:105)
(xxii) "MDR1" (SEQ ID No:18)
(xxiii) "Neurotrypsin" (SEQ ID No:19)
(xxiv) "PTP LOC114971" (SEQ ID No:60)
20 (xxv) "RetSDR2" (SEQ ID No:21)
(xxvi) "SFXN1" (SEQ ID No:24)
(xxvii) "SPC18" (SEQ ID No:26)
(xxiii) "SPC22" (SEQ ID No:27)
(xxix) "SPC25" (SEQ ID No:28)
25 (xxx) "SPTLC2" (SEQ ID No:117)
(xxxi) "stearoyl-CoA desaturase" (SEQ ID No:29)
(xxxii) "STT3" (SEQ ID No:61)
(xxxiii) "TMP21" (SEQ ID No:30)
(xxxiv) "UGCGL1" (SEQ ID No:45)
30 (xxxv) "visinin-like 1" (SEQ ID No:37)
(xxxvi) "Wolframin" (SEQ ID No:67)
(xxxvii) "YME1L1" (SEQ ID No:32)

and wherein the one or more proteins of BACE1 (a) complex are selected from the group consisting of

- 5 (i) "CGI-13" (SEQ ID No:72)
- (ii) "Cadherin EGF LAG seven-pass G-type receptor 2" (SEQ ID No:35)
- (iii) "Calsyntenin 1" (SEQ ID No:36)
- (iv) "Delta-like homolog" (SEQ ID No:118)
- (v) "FLJ30668" (SEQ ID No:69)
- 10 (vi) "FLJ39249" (SEQ ID No:71)
- (vii) "ITCH" (SEQ ID No:73)
- (viii) "KIAA1250" (SEQ ID No:107)
- (ix) "Nicastrin" (SEQ ID No:9)
- (x) "Nogo-A" (SEQ ID No:77)
- 15 (xi) "PDGFRB" (SEQ ID No:78)
- (xii) "PTK7" (SEQ ID No:80)
- (xiii) "SERPINA1" (SEQ ID No:83)
- (xiv) "SIM TO Y71H10A. 2.P" (SEQ ID No:85)
- (xv) "STX10" (SEQ ID No:65)
- 20 (xvi) "Sortilin-related receptor" (SEQ ID No:52)
- (xvii) "Thioredoxin domain-containing protein" (SEQ ID No:101)
- (xviii) "integral membrane transporter protein" (SEQ ID No:114)
- (xix) "kinectin 1 (kinesin receptor)" (SEQ ID No:90), and
- (xx) "BACE1" (SEQ ID No:38),

25

and wherein the one or more proteins of the BACE1 (b) complex are selected from the group consisting of

- (i) "APP" (SEQ ID No:23)
- 30 (ii) "Nicastrin" (SEQ ID No:9)
- (iii) "ACAT1" (SEQ ID No:4)
- (iv) "APLP2" (SEQ ID No:22)
- (v) "BRI" (SEQ ID No:5)

- (vi) "calsyntenin 1 " (SEQ ID No:6)
(vii) "CELSR2" (SEQ ID No:39)
(viii) "CGI-13 " (SEQ ID No:72)
5 (ix) "DLK1" (SEQ ID No:7)
(x) "DSCD75" (SEQ ID No:8)
(ii) "FADS2" (SEQ ID No:40)
(xii) "GPR49" (SEQ ID No:115)
(xiii) "ITM2C" (SEQ ID No:13)
10 (xiv) "KiDins220" (SEQ ID No:17)
(xv) "LAPTM4B " (SEQ ID No:33)
(xvi) "Neurotrypsin" (SEQ ID No:19)
(xvii) "NogoA" (SEQ ID No:41)
(xviii) "OS-9" (SEQ ID No:42)
15 (xix) "PDGFRB" (SEQ ID No:43)
(xx) "PTK7 " (SEQ ID No:44)
(xxi) "RetSDR2" (SEQ ID No:21)
(xxii) "S100alpha" (SEQ ID No:34)
(xxiii) "SORL1" (SEQ ID No:25)
20 (xxiv) "stearoyl-CoA desaturase" (SEQ ID No:29)
(xxv) "TMP21" (SEQ ID No:30)
(xxvi) "UGCGL1" (SEQ ID No:45)
(xxvii) "BACE1" (SEQ ID No:38)
- 25 and wherein the one or more proteins of the Psen2-complex are selected from the group consisting of
- (i) "aph-1a" (SEQ ID No:1)
(ii) "Nicastrin" (SEQ ID No:9)
30 (iii) "CGI-13 " (SEQ ID No:72)
(iv) "DSCD75" (SEQ ID No:8)
(v) "ECSIT" (SEQ ID No:55)
(vi) "FACL3" (SEQ ID No:11)

- (vii) "FADS2" (SEQ ID No:40)
(viii) "FLJ10579" (SEQ ID No:12)
5 (ix) "FLJ20481" (SEQ ID No:82)
(x) "ITPR1" (SEQ ID No:16)
(xi) "KIAA0090" (SEQ ID No:57)
(xii) "MDR1" (SEQ ID No:18)
(xiii) "NicAChRa3" (SEQ ID No:62)
10 (xiv) "PLD3" (SEQ ID No:20)
(xv) "SFXN1" (SEQ ID No:24)
(xvi) "SLC4A2" (SEQ ID No:63)
(xvii) "SORT1" (SEQ ID No:15)
(xviii) "SPC18" (SEQ ID No:26)
15 (xix) "SPC22" (SEQ ID No:27)
(xx) "SPC25" (SEQ ID No:28)
(xxi) "SPTLC2" (SEQ ID No:117)
(xxii) "stearoyl-CoA desaturase" (SEQ ID No:29)
(xxiii) "STT3" (SEQ ID No:61)
20 (xxiv) "TMP21" (SEQ ID No:30)
(xxv) "VLCAD" (SEQ ID No:31)
(xxvi) "Wolframin" (SEQ ID No:67)
(xxvii) "YME1L1" (SEQ ID No:32), and
(xxviii) "Psen2" (SEQ ID No:121)

25

and wherein the at least one protein of PTK7 complex is selected from the group consisting of:

- (i) "APP" (SEQ ID No:23)
30 (ii) "BR1" (SEQ ID No:5)
(iii) "CELSR2" (SEQ ID No:39)
(iv) "DLK1" (SEQ ID No:7)
(v) "FADS2" (SEQ ID No:40)

(vi) "HIFPH3/EGLN3 " (SEQ ID No:64)

(vii) "ITM2C" (SEQ ID No:13)

5 (viii) "Nap1-like " (SEQ ID No:116)

(ix) "Reelin" (SEQ ID No:51)

(x) "PTK7" (SEQ ID No:44)

10 14. The complex of any of claims 12 or 13, wherein one or more of the proteins are present in the form a fusion protein comprising said protein fused to an amino acid sequence different from that of the protein.

15 15. The complex of claim 14, wherein said amino acid sequence is an affinity tag or label.

16. A process for preparing and optionally analyzing a complex of any of claims 12 to 15 or of one or more components thereof comprising the following steps:

20 Expressing a protein of the complex, preferably a tagged protein, in a target cell, isolating the protein complex which is attached to the protein, preferably a tagged protein, and optionally disassociating the protein complex and isolating the individual complex members.

25 17. The process according to claim 16, wherein the tagged protein comprises two different tags which allow two separate affinity purification steps.

18. The process according to any of claims 16 or 17, wherein the two tags are separated by a cleavage site for a protease.

30 19. Nucleic acid construct containing one or more nucleic acids encoding proteins of a complex according to any of claims 12 to 15.

20. Host cell, containing a nucleic acid construct according to claim 19.

- 5 21. A kit comprising in one container the complex of any of claims 12 to 15, optionally together with an antibody against the complex and/or further components such as reagents and working instructions.
- 10 22. The kit according to claim 13 for processing a substrate of a complex of any one of claims 12 to 15.
23. The kit according to any of claims 21 or 22 for the diagnosis or prognosis of a disease or a disease risk, preferentially for a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
- 15 24. Array in which at least a complex according to any of claims 12 to 15 is attached to a solid carrier.
- 20 25. A process for processing a substrate of a complex of any one of claims 12 to 15 comprising the step of bringing into contact a complex to any of claims 12 to 15 with said substrate, such that said substrate is processed.
- 25 26. A pharmaceutical composition comprising the protein complex of any of claims 12 to 15.
27. The pharmaceutical composition according to claim 26 for the treatment of neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
- 30 28. A method for screening for a molecule that binds to the complex of any one of claims 12 to 15, comprising the following steps:
(a) exposing said complex, or a cell or organism containing said complex, to one or more candidate molecules; and

(b) determining whether said candidate molecule is bound to the complex.

5 29. A method for screening for a molecule that modulates directly or indirectly the function, activity, composition or formation of the complex of any one of claims 1 to 7 comprising the steps of:

(a) exposing said complex, or a cell or organism containing said complex to one or more candidate molecules; and

10 (b) determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex.

30. The method of claim 29, further comprising the step of determining whether said candidate molecule modulates gamma secretase and/or beta secretase activity.

15

31. The method of any of claims 29 or 30, wherein the amount of said complex is determined.

20 32. The method of any of claims 29 or 30, wherein the activity of said complex is determined.

25 33. The method of claim 32, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.

30

34. The method of claim 33, wherein the substrate is APP and the cleavage of APP is analyzed.

35. The method of any of claims 29 or 30, wherein the amount of the individual protein components of said complex are determined.
- 5 36. The method of claim 35, wherein said determining step comprises determining whether any of the proteins of the respective complex as defined in claim 13 is present in the complex.
- 10 37. The method of any of claims. 29 to 36, wherein said method is a method of screening for a drug for treatment or prevention of neurodegenerative disease such as Alzheimer's disease.
- 15 38. Use of a molecule that modulates the amount of, activity of, or the protein components of the complex of any one of claims 1 to 7 for the manufacture of a medicament for the treatment or prevention of a neurodegenerative disease such as Alzheimer's disease.
- 20 39. The use according to claim 38, wherein the modulating molecule is a FADS2 interacting molecule, preferably a FADS2 inhibitor.
40. The use according to claim 39, with the features as defined in claims 2 to 6.
- 25 41. A method for the production of a pharmaceutical composition comprising carrying out the method of any of claims 28 to 37 and further comprising mixing the identified molecule with a pharmaceutically acceptable carrier.
- 30 42. A method for diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject, which disease or disorder is characterized by an aberrant amount of, component disposition of, or intracellular localization of the complex of any one of claims 12 to 15, comprising determining the amount of, activity of, protein components of, and/or intracellular localization of, said complex.

43. The method of claim 42, wherein the activity of gamma secretase and/or beta secretase is determined.
- 5
44. The method of any of claims 42 or 43, wherein the amount of said complex is determined.
45. The method of any claim 42 or 43, wherein the activity of said complex is determined.
- 10
46. The method of claim 45, wherein said determining step comprises isolating from the cell or organism said complex to produce said isolated complex and contacting said isolated complex in the presence or absence of a candidate molecule with a substrate of said complex and determining whether said substrate is processed in the absence of the candidate molecule and whether the processing of said substrate is modified in the presence of said candidate molecule.
- 15
47. The method of any of claims 42 or 43, wherein the amount of the individual protein components of said complex are determined.
- 20
48. The method of claim 47, wherein said determining step comprises determining whether any of the proteins according to claim 13 is present in the complex.
- 25
49. The complex of any one of claims 12 to 15, for use in a method of diagnosing a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.
- 30
50. A method for treating or preventing a disease or disorder characterized by an aberrant amount of, activity of, component composition of or intracellular localization of, the complex of any one of claims 12 to 15, comprising administering to a subject in need of such treatment or prevention a therapeutically

effective amount of one or more molecules that modulate the amount of, activity or, or protein components of, said complex.

5

51. The method according to claim 50, wherein the modulating molecule is a FADS2 interacting molecule, preferably a FADS2-inhibitor.

10

52. The method according to claim 51, with the features as defined in any of claims 2 to 6.

53. The method according to any of claims 50 to 52, wherein said disease or disorder involves decreased levels of the amount or activity of said complex.

15

54. The method according to any of claims 50 to 53, wherein said disease or disorder involves increased levels of the amount or activity of said complex.

20

55. The complex of any of claims 12 to 15 as a target for an active agent of a pharmaceutical, preferably a drug target in the treatment or prevention of a disease or disorder, preferentially of a disease or disorder such as neurodegenerative disease such as Alzheimer's disease and related neurodegenerative disorders.

25

56. Use of a FADS2 interacting molecule for the modulation of beta secretase and/or gamma secretase activity in vitro.

FIGURE 1

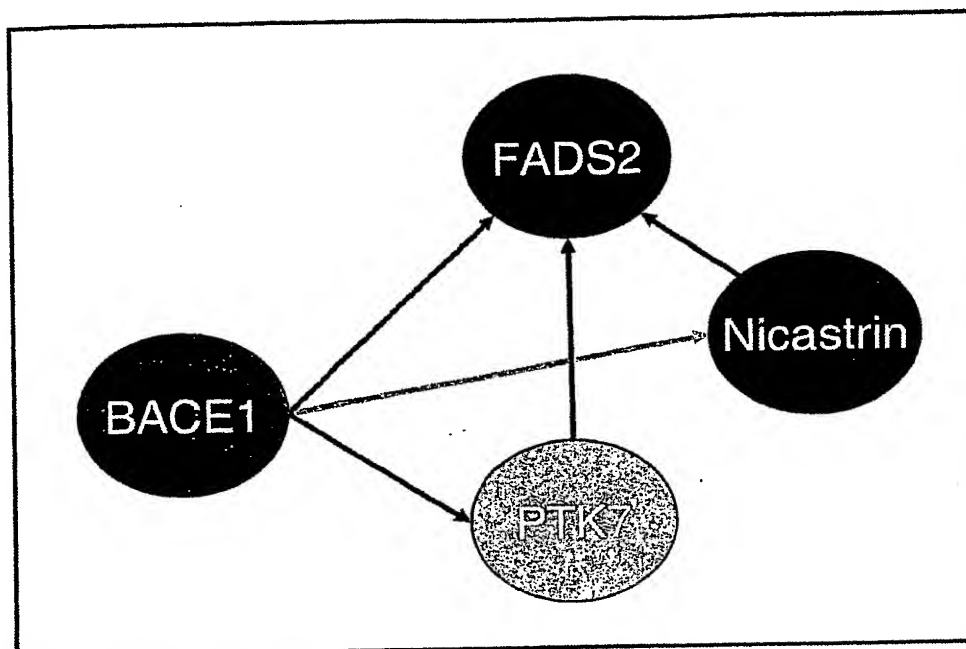


FIGURE 2

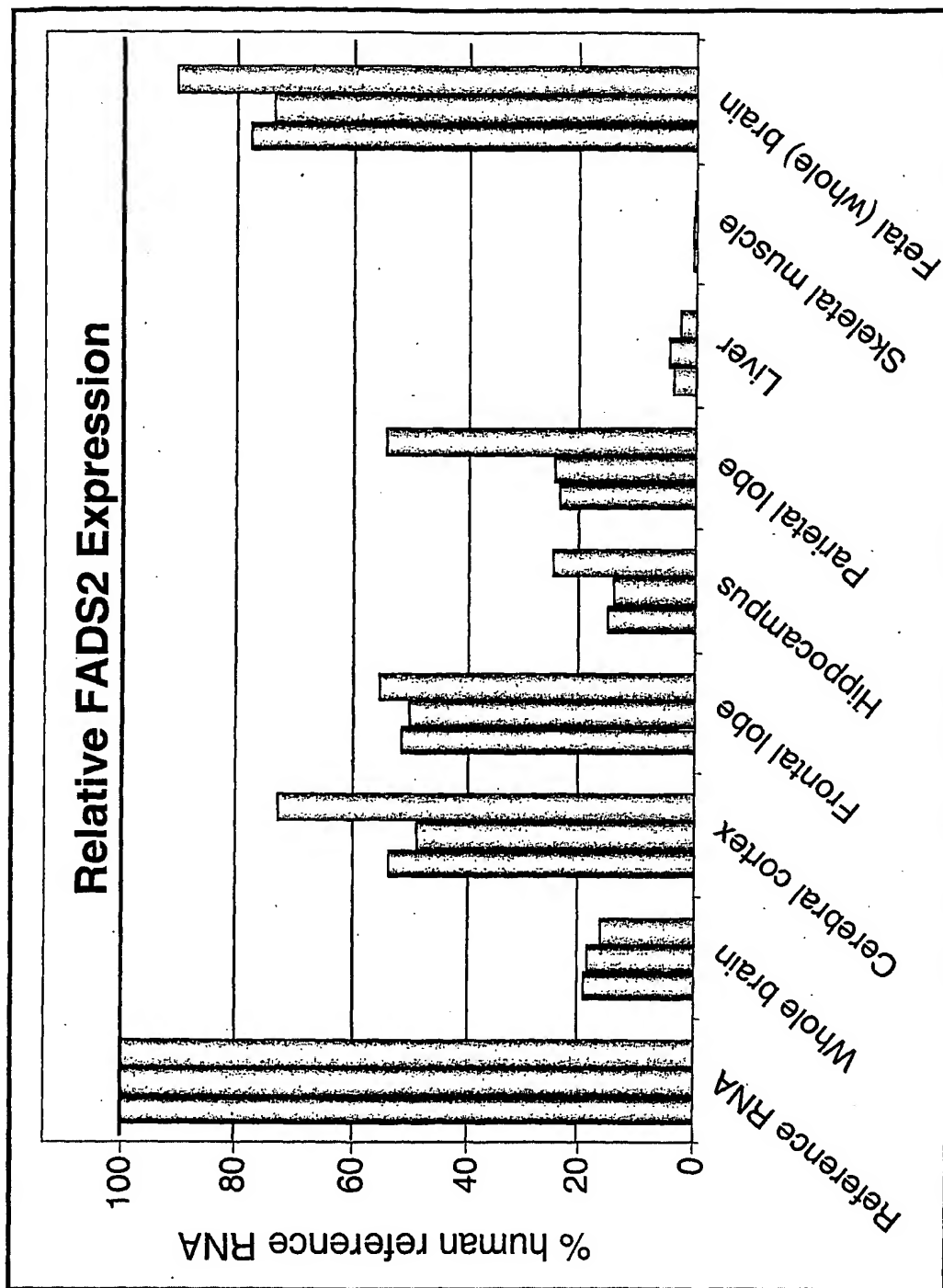


FIGURE 3 A

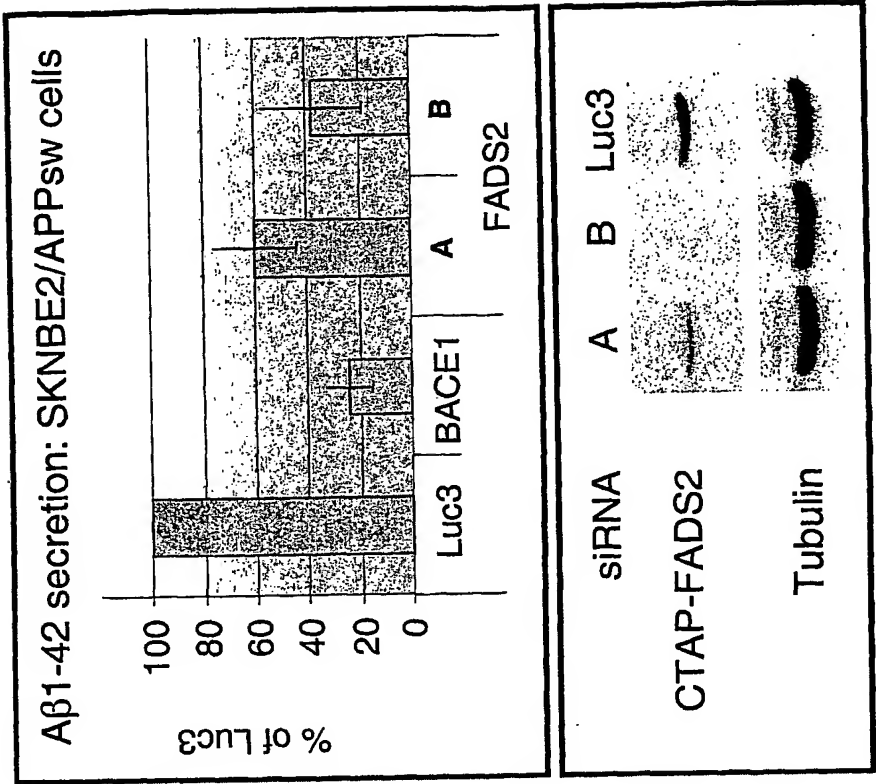


FIGURE 3 B

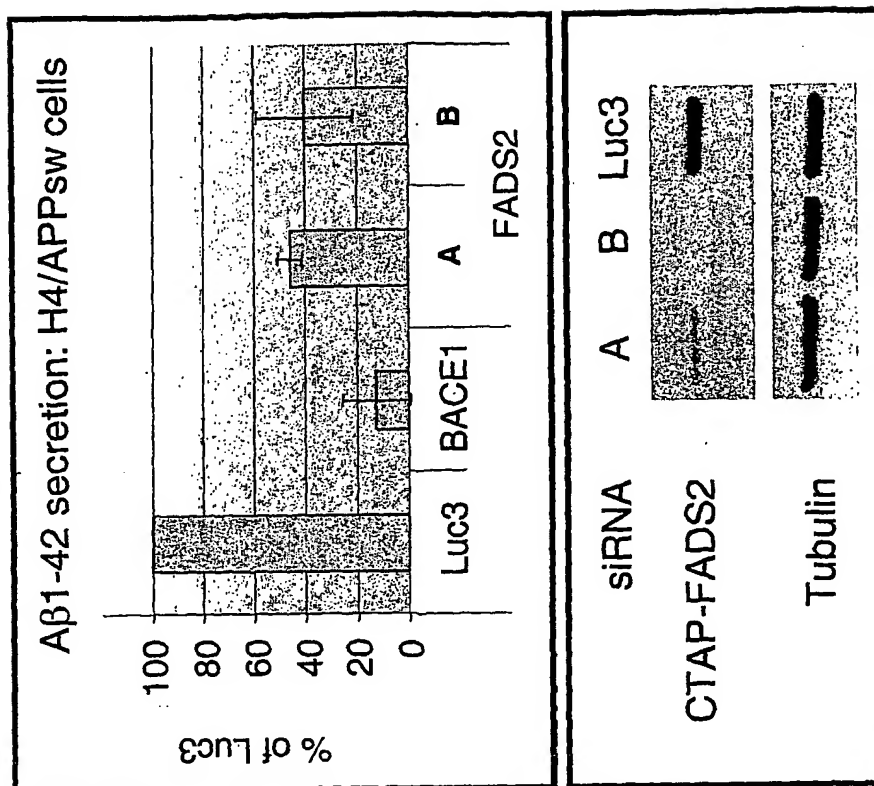


FIGURE 4

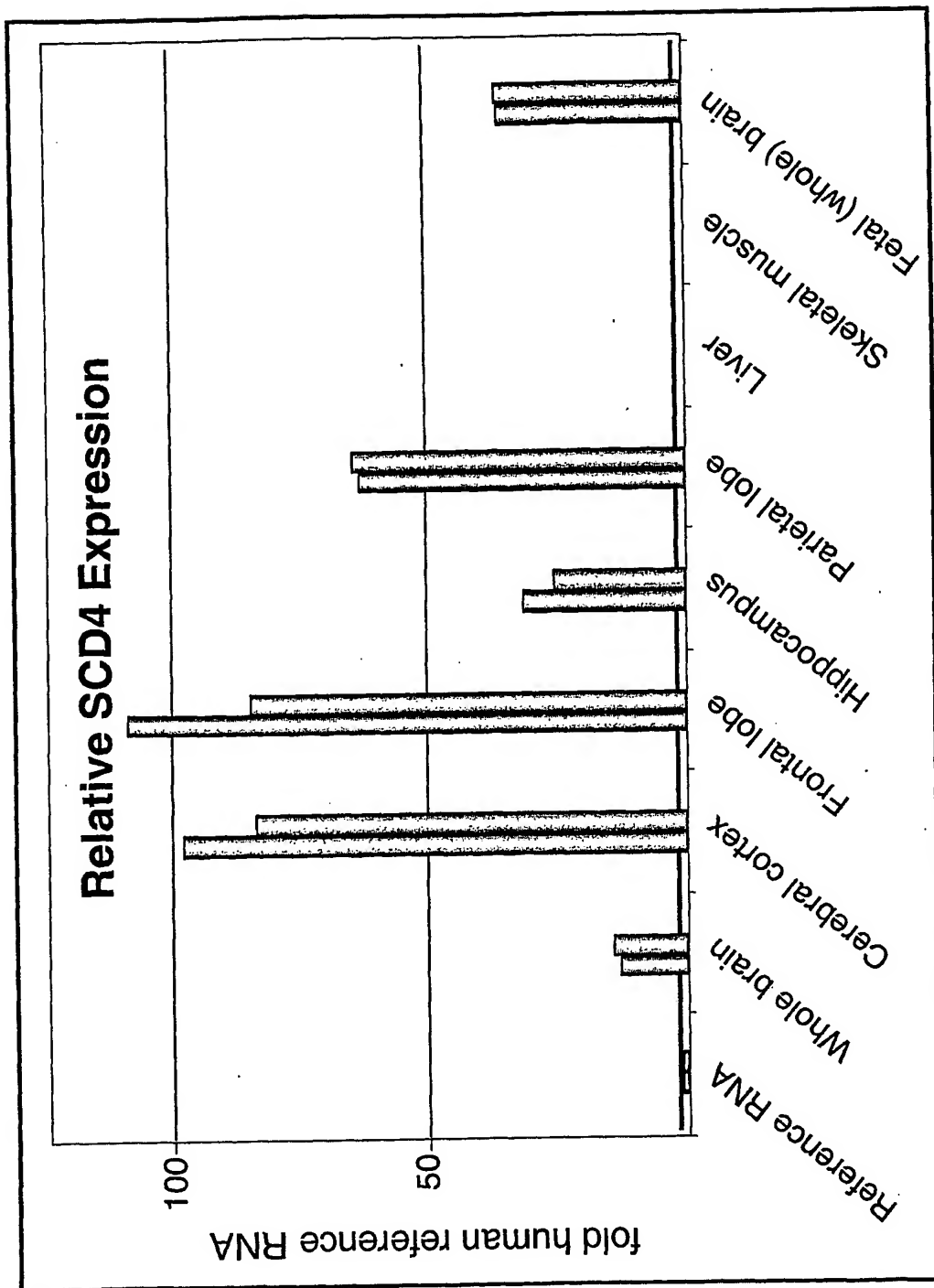


FIGURE 5

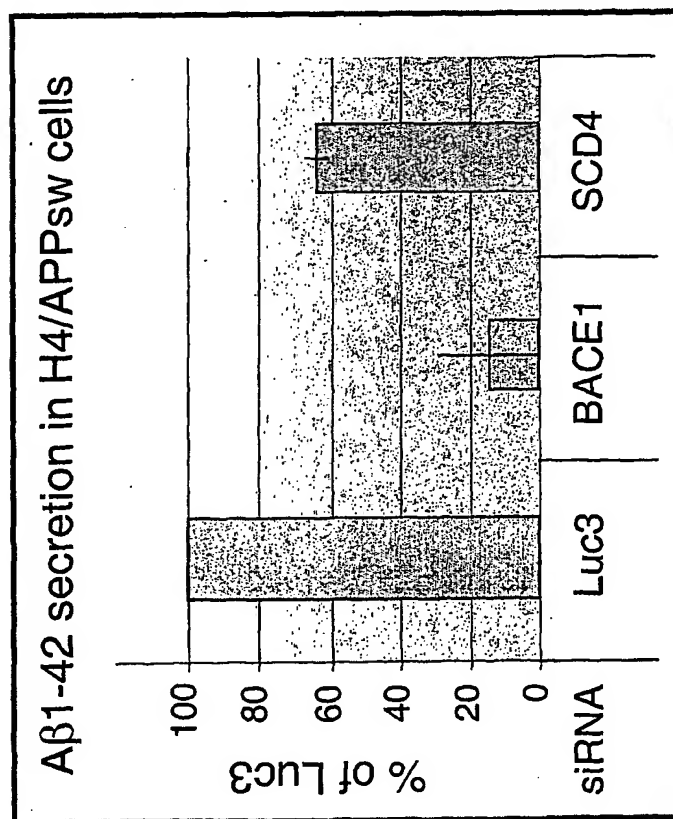
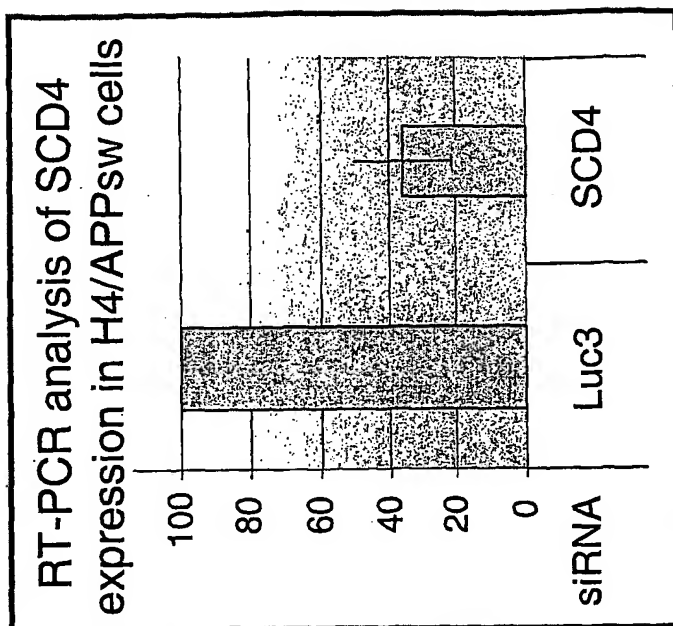


FIGURE 6

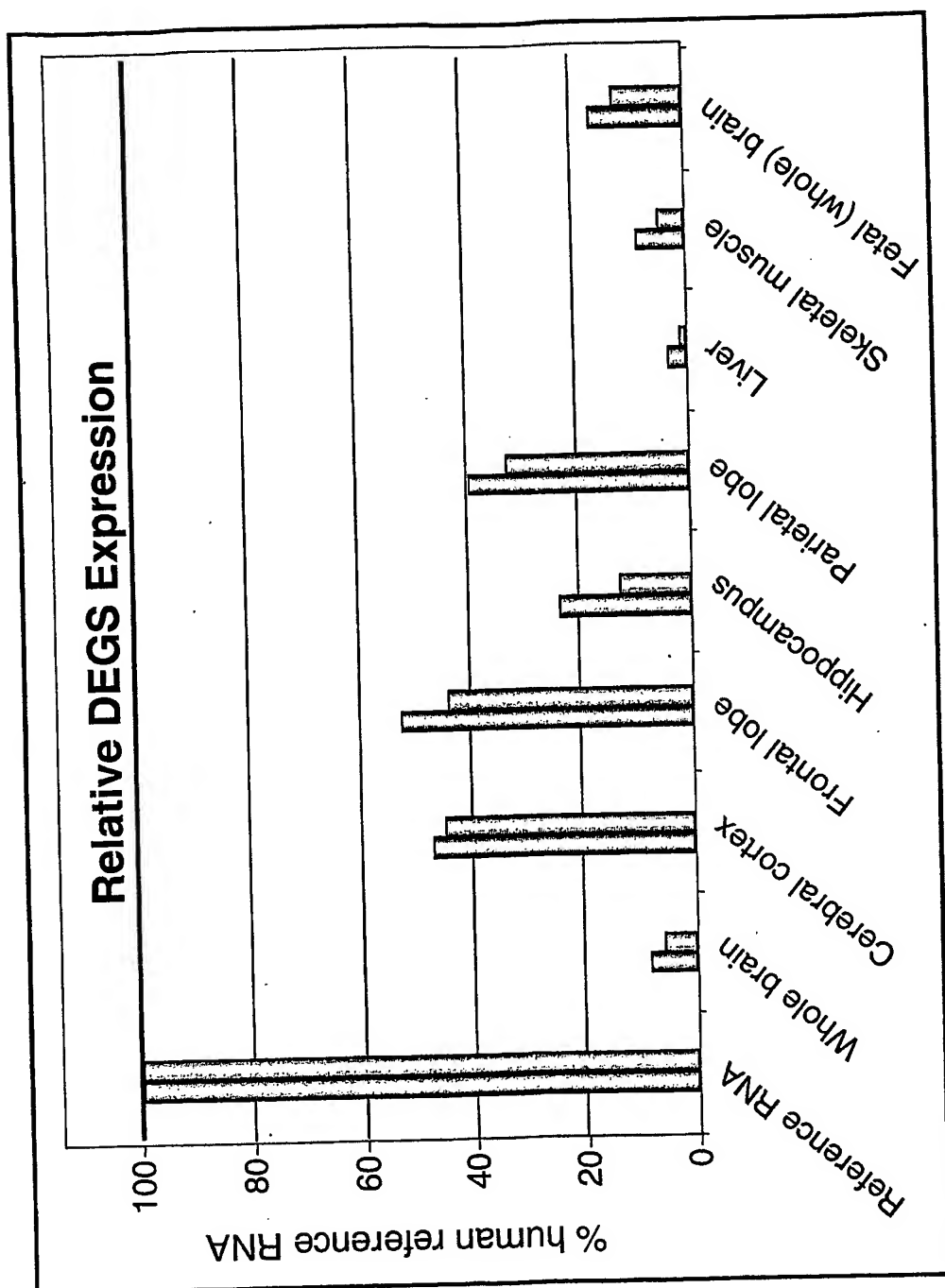
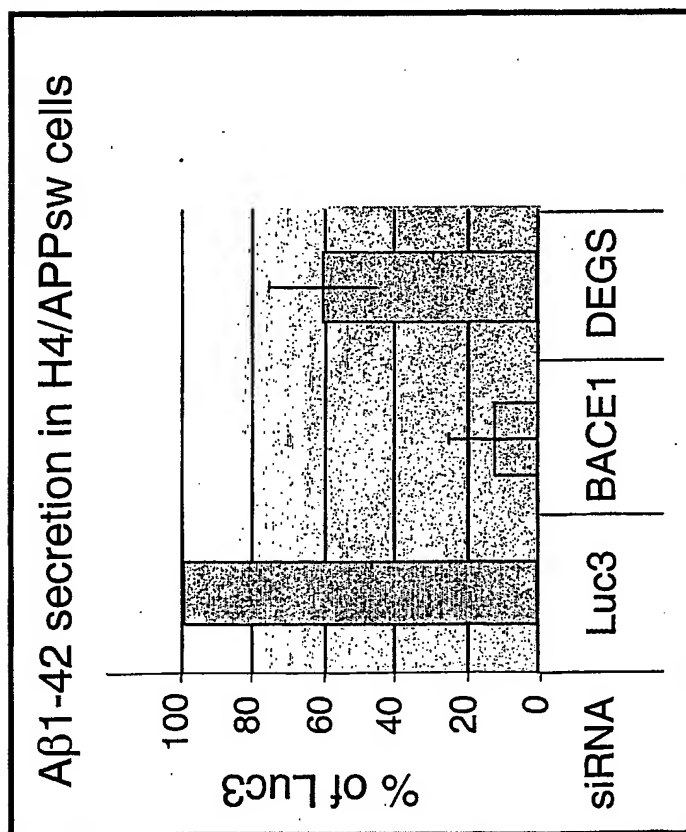
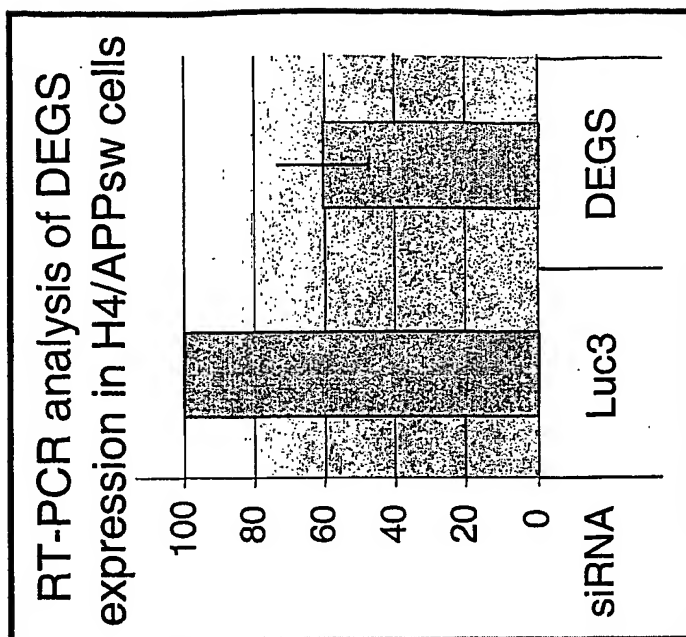


FIGURE 7



SEQUENCES

SEQ ID No:1 (Aph-1a)

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVILVAGAFFWLVSLLLASVWWFIL
5 VHVTDERSDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEGRSPI
SIRQMA YVSGLSFGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAILLH
TFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGL
WAFITAGGSLRSIQRSLLCRRQEDSRVMVYSALRIPPED

10 SEQ ID No: 2 (JUP)

EVMNLMEQPIKVTEWQQTYTYDSGIHSGANTCVPSVSSKGIMEEDEACGRQYTLK
KTTTYTQGVPPSQGDLEYQMSTTARAKRVREAMCPGVSSEGQLALLATQVEGQA
TNLQRLAEPSQLLKSIVHLINYQDDAELVTRALPELTKLLNDEDPVVVTKAAMIV
NQLSKKEASRRALMGSPQLVAAVVRTMQNTSDLDTARCTTSILHNLSSHREGLLA
15 IFKSGGIPALVRMLSSPVESVLFYAITTLHNLLLYQEGAKMACAGRRAQKMVPLL
NKNNPKFLAITTDCLQLLAYGNQESKLILANGGPQALVQIMRNYSYEKLLWTTSR
VLKVLVCPSPNKPAIVEAGGMQALGKHLTSNSPRLVQNCLWTLRNLSDVATKQE
GLESVLKILVNQLSVDDVNVLT CATGTLSNLT CNNSKNKTLVTQNSGVEALIHAIL
RAGDKDDITEPAVCALRHLSRHPEAEMAQNSVRLNYGIPAIVKLLNQPNQWPLV
20 KATIGLIRNLALCPANHAPLQEA AVIPRLVQLLVKAHQDAQRHVAAGTQQPYTDG
VRMEEIVEGCTGALHILARDPMNRMEIFRLNTIPLFVQLLYSSVENIQRVAAGVLC
ELAQDKEAADAIDAEGASAPLMELLHSRNEGTATYAAAVLFRISEDKNPDYRKR
SVELTNSLFFKHDPAAWEAAQSMIPINEPYGDDMDATYRPMYSSDVPLDPLEMHM
DMDGDYPIDTYS DGLRPPYPTADHMLA

25

SEQ ID No: 3 (Psen1)

MTELPAPLSYFQNAQMSDNHLSNTVRSQNDNRERQEHNDRRSLGHPEPLSNGRP
QGNSRQVVEQDEEED EELTKYGAKHVIMLFVPVTLCMVVVVATIKSVSFYTRKD
GQLIYTPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVVLKYRCYKVIHAWLII
30 SSSLLLFFFSFIYLG EVFKTYNVAVDYITVALLIWNFGVVGMSIHWKGPLRLQQAY
LIMISALMALVFIKYLPEWTAWLLAVISVYDLVAVLCPKGPLRMLVETAQERNET
LFPALIYSSTMVWLVNMAEGDPEAQRVSKNSKYNAESTERESQDTVAENDDGG

FSEWEAQRDShLGPHRSTPESRAAVQELSSSILAGEDPEERGVKLGLGDFIFYSVL
VGKASATASGDWNTTIACFVAILIGLCLTLLLAIFKKALPALPISITFGLVFYFATD
YLVQPFMDQLAFHQFYI

5 SEQ ID No: 4 (ACAT1)

MVGEEKMSLRNRLSKSRENPEEDEDQRNPAKESLETSPNGRIDIKQLIAKKIKLTAE
AEARLKPPFFMKEVGSHFDDFVTNLIEKSASLDNGGCALTTFVLEGEKNNHRAKD
LRAPPEQGKIFIARRSLDELLEVDHIRTYYHMFIALLLFILSTLVVDYIDEGRLVLE
FSLLSYAFGKFPTVVWTWWIMFLSTFSVPYFLFQHWATGYSSSHPLIRSLFHGFL
10 FMIFQIGVLGFGPTYVVLAYTLPPASRFIIIEQIRFVMKAHSFVRENVPRLNSAKE
KSSTVPIPTVNQYLYFLFAPTLIYRDSYPRNPTVRWGYVAMKFAQVFGCFFYVYYI
FERLCAPLFRNIKQEPFSARVLVLCVFNSILPGVLILFLTFFAFLHCWLNFAEMLRF
GDRMFYKDWWNSTSYSNNYRTWNVVDWLYYYAYKDFLWFFSKRFKSAAM
LAVFAVSAVVHEYALAVCLSFFYPVLFVLFMFFGMAFNFTVND SRKKPIWNVLM
15 WTSFLGNGVLLCFYSQEWYARQHCPLKNPTFLDYVRPRSWTCRYVF

SEQ ID No: 5 (BRI)

MVKVTFNSALAQKEAKKDEPKSGEEALIIPDAVAVDCKDPDDVVPVGQRRWC
WCMCFGLAFMLAGVILGGAYLYKYFALQPDDVYYCGIKYIKDDVILNEPSADAPA
20 ALYQTIEENIKIFEEEEVEFISVPVPEFADSDPANIVHDFNKKLTAYLDLNLDKCYVI
PLNTSIVMPPRNLELLINIKAGTYLPQSYLIHEH MVITDRIENIDHLGFFTYRLCHDK
ETYKLQRRETIKGIQKREASNCFAIRHFENKFAVETLICS

SEQ ID No: 6 (calsyntenin 1)

MLRRPAPALAPAARLLLAGLLCGGGVWAARVNKHKPWLEPTYHGIVTENDNTVL
25 LDPPLIALDKDAPLRFAGEICGFKIHGQNVPFDAVVVDKSTGEGVIRSKEKLDCEL
QKDYSFTIQAYDCGKGPDTNVKKSHKATVHIQVNDVNEYAPVFKEKSYKATVIE
GKQYDSILRVEAVDADCSPQFSQICSYEITPDVPFTVDKDG YIKNTEKLN YGKEHQ
YKLTVTAYDCGKKRATEDVLVKISIKPTCTPGWQGWNNRIEYEPGTGALAVFPNI
30 HLETCDEPVASVQATVELETSHIGKGC DRD TYSEKSLHRLCGAAAGTAELLPSPSG
SLNWTMGLPTDNGHDS DQVFEFNGTQAVRIPDGVVSVSPKEPFTISVWMRHGPF
RKKETILCSDKTD MNRRHYSLYVHGCRLIFLFRQDPSEEKKYRPAEFHWKLNQV

CDEEWHHYVLNVEFPSVTLYADGTSHEPFSVTEDYPLHPSKIETQLVVGACWQEF
SGVENDNETEPVTVACAGGDLHMTQFFRGNLAGLTLRSGKLADKKVIDCLYTCK
EGLDLQVLEDSGRGVQIQAHRSQLVLTLEGEDLGELDKAMQHISYLSNRQFPTPGI
RRLKITSTIKCFNEATCISVPPVDGYVMVLQPEEPKISLSGVVHFAAASEFESSEGV
5 FLFPELRIISTITREVEPEGDGAEDPTVQESLVSEEIVHDLDTCEVTVEGEELNHEQE
SLEVDMARLQKKGIEVSSSELGMTFTGVDTMASYEEVLHLLRYRNWHARSLLDR
KFKLICSELNGRYSISNEFKVEVNVHTANPMEHANHMAAQPQFVHPEHRSFVDLS
GHNLANPHFPAVVHSTATVVIVVCVSSLVFMILGVFRIRAAHRRTMRDQDTGKE
NEMDWDDSAITITVNPMEYEDQHSSEEEEEEEEEEESEDGEEEDDITSAESESSEE
10 EEQEQQDPQNATRQQQLEWDDSTLSY

SEQ ID No: 7 (DLK1)

MTATEALLRVLLLLLAFGHSTYGAECFPACNPQNGFCEDDNVCRCQPGWQGPLC
DQCVTSPGCLHGLCGEPGQCICTDGWDGELCDRDVRACSSAPCANNGTCVSLDG
15 GLYECSCAPGYSGKDCQKKDGPCVINGSPCQHGGTCVDDEGRASHASCLCPPGFS
GNFCEIVANSCTPNPCENDGVCTDIGGDFRCRCPAGFIDKTCSRPVTNCASSPCQN
GGTCLQHTQGQAICFTILGVLTSLVVLGTVGIVFLNKCETWVSNLRYNHMLRKKK
NLLLQYNSGEDLA VNIIFPEKIDMTTFSKEAGDEEI

20 SEQ ID No: 8 (DSCD75)

MLGLLVALLALGLAVFALLDVWYLVRLPCAVLRARLLQPRVRDLLAEQRFPGRV
LPDLDLLLHMNNARYLREADFARVAHLTRCGVLGALRELRAHTVLAASCARHR
RSLRLLEPFVTRLLGWDDRAFYLEARFVSLRDGFVCALLRFRQHLLGTSPERVV
QHLCQRRVEPPELPADLQHWISYNEASSQLLRMESGLSDVTKDQ

25

SEQ ID No:9 (Nicastrin)

MATAGGGSGADPGSRGILLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLNA
THQIGCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLSKHFTRDLMEKL
KGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVYSNSYGPEFAHCREIQWNSL
30 GNGLAYEDFSFIFLLEDENETKVIKQCYQDHNLSQNGSAPTFFLCAMQLFSHMLA
VISTATCMRRSSIQSTFSINPEIVCDPLSDYNVWSMLKPINTTGTLKPDDR VVVAAT
RLDSRSFFWNVAPGAESA VASFVTQLAAAEALQKAPDVTTLP RNVMFVFFQGETF

DYIGSSRMVYDMEKGKFPVQLENVDSFVELGQVALRTSLELWMHTDPVSQKNES
VRNQVEDLLATLEKSGAGVPAVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHS
GAFHNKYYQSIYDTAENINVSYPEWLSPEEDLNFVTD TAKALADVATVLGRALYE
LAGGTNFSDTVQADPQTVTRLLYGFLIKANNSWFQSILRQDLRSYLGDGPLQHYYA
5 VSSPTNTTYVVQYALANLTGTVVNLTREQCQDPSKVPSENKDLYEYSWVQGPLHS
NETDRLPRCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFLIASKEL
ELITLTVGFGILIFSLIVTYCINAKADVLFAPREPGAVSY

SEQ ID No:10 (Pen-2)

10 MNLERVSNEEKLNLCKRYYLGGFAFLPFLWLVNIFWFFREAFVLPAYTEQSQIKG
YVWRS AVGFLFWVIVLT SWITIFQIYRPRWGALGDYLSFTIPLGTP

SEQ ID No: 11 (FACL3)

MNNHVSSKPSTMKLKHTINPILLYFIHFLISLYTILTYIPFYFFSESROEKS NR IKA KP
15 VNSKPDSAYRSVNSLDGLASVLYPGCDTLDKVFTYAKNKFKNKRL LGTREV LNEE
DEVQPNGKIFKKVILGQYNWLSYEDVFVRAFNFNGNLQMLGQKPKTNIAIFCETR
AEWMIAAQACFMYNFQLVTLYATLGGAIVHALNETEVTNITSKELLQTKLKDIV
SLVPRLRHITVDGKPPTWSDFPKGIVHTMAAVEALGAKASMENQPHSKPLPSDIA
VIMYTSGSTGLPKGVMISHSNIIAGITGMAERIPELGEEDVYIGYLPLAHVLELSAEL
20 VCLSHGCRIGYSSPQTLADQSSKIKKGSKGDTSM LKPTLMAAVPEIMDRIYKNVM
NKVSEMSSFQRNLFILAYNYKMEQISKGRNTPLCDSFVFRKVRSLG GNIRLLLCG
GAPLSATTQRFMNICFC CPVGQGYGLTESAGAGTISEVWDYNTGRVGAPLVCCEI
KLKNWEEGGYFN TDKPHPRGEILIGGQSVTMGYKNEAKTKADFSE DENGQRWL
CTGDIGEFEPDGCLKIIDRKKDLVKLQAGEYVSLGKVEAALKNLPLVDNICAYANS
25 YHSYVIGFVVPNQKELTELARKKGLKGTWEELCNSCEMENEVLKVLSEAAISASL
EKFEIPVKIRLSPEPWT PETGLVTDAFKLKRKELKTHYQADIERMYGRK

SEQ ID No: 12 (FLJ10579)

MSRLGALGGARAGLGLLLGTAAGLGFLCLLYSQRWKRTQRHGRS QSLPNSLDYT
30 QTSDPGRHVMLLRAVPGGAGDASVLP SLPREGQEKVLDRLDFVLTSLVALRREVE
ELRSSLRGLAGEIVGEVRCHMEENQRVARRRRFPFVRERSDSTGSSSVYFTASSGA
TFTDAESEGGYTTANAESDNERDSDKESEDGEDEVSCETVKMGRKDSLDEEEAA

SGASSALEAGGSSGLEDVLPLLQQADELHRGDEQGKREGFQLLLNNKLVYGSQRD
FLWRLARAYSDMCELTEEVSEKKSYALDGKEEAEEAALEKGDESADCHLWYAVLC
GQLAEHESIQRRIQSGFSFKEHVDKAIALQPENPMAHFLGRWCYQVSHLSWLEK
KTATALLESPLSATVEDALQSFLKAEELQPGFSKAGRVYISKCYRELGKNSEARW
5 WMKLALELPDVTKEDLAIQKDLEEEVILRD

SEQ ID No: 13 (TTM2C)

MVKISFQPAVAGIKGDKADKASASAPAPASATEILLTPAREEQPPQHRSKRGGSVG
GVCYLSMGMVVLLMGLVFASVYTYRYFFLAQLARDNFFRCGVLYEDSLSSQVRT
10 QMELEEDVKIYLDENYERINVPVPQFGGGDPADIIHDFQRGLTAYHDISLDKCYVIE
LNTTIVLPPRNFWEELLMNVKRGTYLPQTYIIQEEMVVTEHVSDEALGSFIYHLCN
GKDTYRLRRRATRRRINKRGAKNCNAIRHFENTFVVETLICGVV

SEQ ID No:14 (Presenilin)

15 MTELPAPLSYFQNAQMSEDNHLSTNDNRERQEHNDRRSLGHPEPLSNRPPQNS
RQVVEQDEEEDDEELTKYGAHVIMLFVPVTLCMVVVVATIKSVSFYTRKDGQLI
YTPFTEDTETVGQRALHSILNAAIMISVIVVMTILLVLYKYRCYKVIHAWLISSLL
LLFFFSFIYLGEVFKTYNVAVDYITVALLIWNLGVVGMISIIHWKGPLRLQQAYLIMI
SALMALVFIKYLPEWTAWLILAVISVYDLVAVLCPKGPLRMLVETAQERNETLFP
20 ALIYSSTMVWLVNMAEGDPEAQRRVSKNSKYNAESTERESQDTVAENDDGGFSE
EWEAQRDShLGPHERSTPESRAAVQELSSSILAGEDPEERGVLGLGDFIFYSVLVG
KASATASGDWNTTIACFVAILIGLCLTLLLAIFKKALPALPISITFGLVFYFATDYL
VQPFMDQLAFHQFYI

25 SEQ ID No:15 (Sortilin/Sort1)

MERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRLDAPPPPAAPLPRWSGPIGV
SWGLRAAAAGGAFPRGGRWRRSAPGEDEECGRVRDFVAKLANNTHQHVFDDL
GSVLSWVG DSTGVILVLTTFHVPLVIMTFGQSKLYRSEDYGNFKDITDLINNTFI
RTEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTDLPFHPLTQMM
30 YSPQNSDYLLALSTENGLWVSKNFGGKWEIHKAVCLAKWGSNTIFFTTYANGS
CKADLGALELWRTSDLGKSFKTIGVKIYSFGLGGRFLFASVMADKDTTRRIHVSTD
QGDTWSMAQLPSVGQEYFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS

KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITFDQGGRWTHLRKP
ENSECDATAKNKNECSLHHASYSISQKLNVPMAPLSEPNAVGVIAHGSVGD AISV
MVPDVYISDDGGYSWTKMLEGPHYTYTLDSSGGIIVAIEHSSRPINVIKFSTDEGQCW
QTYTFTTRDPIYFTGLASEPGARSMNISTWGFTESFLTSQWVSYTIDFKDILERNCEEK
5 DYTIVLAHSTDPEDYEDGCILGYKEQFLRLRKSSMCQNGRDYVVTKQPSICLCSLE
DFLCDFGYRPPENDSKCVEQPELKGHDLFCLYGREEHLTTNGYRKIPGDKCQGG
VNPVREVKDLKKKCTSNFLSPEKQNSKSNVPIILAIVGLMLVTVVAGVLIVKKYV
CGGRFLVHRYSVLQQHAEANGVDGVDALDTASHTNKSGYHDDSDLEDLLE

10 SEQ ID No: 16 (ITPR1)

MSDKMSSFLHIGDICS LYAEGSTNGFISTLGLVDDRCVVQPETGDLNNPPKKFRDC
LFKLCPMNRYS AQKQFWKA AKPGANSTTDAVLLNKLHHAADLEKKQNETENRK
LLGTVIQYGNVIQLLHLKSNKYLTVNKRLPALLEKNAMRVTLDEAGNEGSWFYIQ
PFYKLR SIGDSVVIGDKVVLNPNVAGQPLHASSHQLVDNPGCNEVNSVNCNTSWK
15 IVLFMKWSDNKDDILKGGDVVRLFHAEQEKFLTCD EHRKKQH VFLRTTGRQSATS
ATSSKALWEVEVVQH DPCRGGAGYWN SLFRFKHLATGHYLA AEVDPDFEEECLE
FQPSVDPDQDASRSRLRNAQEKMVYSLVS VPEGNDISSIFELDP TTLRGGDSL VPR
NSYVRLRHLCTNTWVHSTNIPIDKEEEKPVMLKIGTSPVKEDKEAFAIVPVSPA EV
RDLD FANDASKVLGSIAGKLEKGTITQNERRSVTKLLEDLVYFVTGGTNSGQDVL
20 EVVFSKPNRERQKLMREQNILKQIFKLLQAPFTDCGDGPMLRLEELGDQRHAPFR
HICRLCYRVL RHSQQDYRKNQEYIAKQFGFMQKQIGYDVLAEDTITALLHNNRKL
LEKHITAAEIDTFVSLVRKNREPRFLDYLS DLCVSMNKSIPVTQELICKAVLNPTNA
DILIETKLVL SRFEFEGVSSTGENALEAGEDEEEVWLFWRDSNKEIRSKSVRELAQD
AKEGQKEDRDVLSYYRYQLNLFARMCLDRQYL AINEISGQLDVDLILRCMSDENL
25 PYDLRASFCRLMLHMHVDRDPQEQVTPVKYARLWSEIPSEIAIDDYDSSGASKDEI
KERFAQTMEFVEEYLRDVVCQRFPFSDKEKNKLT FEVVNLARNLIYFGFYNFSDLL
RLTKILLAILDCVHVTTIFPISKMAKGEENKGNNDVEKLKSSNVMRSIHGVGELMT
QVVLRGGGFLPMT PMAAAPEGNVKQAEPEKEDIMVMDTKLKIIELQFILNVRLDY
RISCLLCIFKREFDESNSQTSETSSGNSSQEGPSNVP GALDFEHIEEQAE GIFGGRKV
30 YFHEENTPLDLDHGGRTFLRVLLH LTMHDY PPLVSGALQLLFRHFSQRQEV LQA
FKQVQLLVTSQD VDN YKQIKQDLDQLRSIVEKSELWVYKGQGPDETMDGASGEN
EHKKTEEGNNKPQKHESTSSYNYRVVKEILIRLSKLCVQESASVRKSRKQQQRLLR

NMGAHAVVLELLQIPYEKAEDTKMQEIMRLAHEFLQNFCAGNQQNQALLHKHIN
LFLNPGILEAVTMQHIFMNNFQLCSEINERVVQHFVHCIETHGRNVQYIKFLQTTVK
AEGKFIKKCCQDMVMAELVNSGEDVLVFYNDRASQTLIQMMRSEDRMDENSPL
MYHIHLVELLAVCTEGKNVYTEIKCNSLLPLDDIVRVVTHEDCIPEVKIAYINFLNH
5 CYVDTEVEMKEIYTSNHMWKLFENFLVDICRACNNTSDRKHADSILEKYVTEIVM
SIVTTFFSSPFSQSTTLQTRQPVFVQLLQGVFRVYHCNWLMP SQKASVESCIRVLS
DVAKSRAIAIPVDLDSQVNNLFLKSHSIVQKTAMNWRLSARNAARRDSVLAASRD
YRNIIRLQDIVSALEDRLRPLVQAELSVLVDVLHRPELLFPENTDARRKCESGGFI
CKLIKHTKQLLEENEEKLCIKVLQTLREMMTKDRGYGEKLISIDELDNAELPPAPD
10 SENATELESPPLRQLEDHKRGEALRQVLVNRYYGNVRPSGRRESLTSFGNGPLS
AGGPGKPGGGGGSGSSSMSRGEMSLAEVQCHLDKEGASNLVIDLIMNASSDRVF
HESILLAIALLEGGNTTIQHSFFCRLTEDKKSEKFFKV FYDRMKVAQQEIKATVTVN
TSDLGNKKKDDDEVDRDAPSRKKAKEPTTQITEEVRDQLEASAATRKAFTTFRRE
ADPDDHYQPGEQTATADKAKDDLEMSAVTTIMQPILRFLQLLCENHNRLDQNFL
15 RCQNNKTNYNLVCETLQFLDCICGSTTGGLGGLLYNEKNVALINQTLLESLTEYC
QGPCHENQNCIATHESNGIDIITALILNDINPLGKKRMDLVLELKAKNASKLLAIM
ESRHSSENAERILYNMRPKELVEVIKKAYMQGEVEFEDGENGEDGAASPRNVGH
NIYILAHQLARHNKELQSMLKPGGQVDGDEALEFYAKHTAQIEIVRLDRTMEQIVF
PVPSICEFLTKE SKLR IYYTTERDEQGSKINDFFLRSEDLFNEMNWQKKLRAQPVL
20 YWCARNMSFWSSISFNLA VLMNLLVAFFYPFKGV RGGTLEPHWSGLLWTAMLIS
LAIVIALPKPHGIRALIASTILRLFSVGLQPTLFLLGAFNVCNKIIFLMSFVGNCGTFT
RGYRAMVLDVEFLYHLLYL VICAMGLFVHEFFYSLLLFDLVYREETLLNVIKSVTR
NGRSIILTAVLALILVYLF SIVGYLFFKDDFILEVDRLPNETAVPETGESLASEFLSD
VCRVESGENC SSPAPREELVPAEETE QDKEHTCETLLMCIVTVLSHGLRSGGGVGD
25 VLRKPSKEEPLFAARVIYDLLFFFMVIII VLNLI FGVIIDTFADLRSEKQKKEEILKTT
CFICGLERDKFDNKT VTFEEHIKEEHNMWHYLCFIVLVKV KDSTEYTGPE SYVAE
MIKERNLDWFPRMRAMSLVSSDSEGEQNELRNLQEKLESTMKLVTNLSGQ LSELK
DQMTEQRKQKQRIGLLGHPPHMNVNPPQPA

30 SEQ ID No: 17 (KiDins220)

LQLSVKMSVLISQSVINYVEEENIPALKALLEKCKDVDERNECGQTPLMIAAEQGN
LEIVKELIKNGANCNLEDLDNWTALISASKEGHVHIVEELLKCGVNLEHRDMGGW

TALMWACYKGRD VVELLLSHGANPSVTGLYSVYPIIWAAGRGHADIVHLLLQN
GAKVNCSDKYGTTPLVWAARKGHLECVKHLLAMGADV DQEGANSMTALIVAV
KGGYTQSVKEILKRNPVNLT DKGNTALMIASKEGHT EIVQDLLDAGTYVNIPD
RSGDTV LIGAVRGGHVEIVRALLQKYADIDIRGQDNKTALYWAVEKGNATMVRD
5 ILQCNPDTEICTKDGETPLIKATKMRNIEVVELL DKGAKVSAVDKKGDTPLHIAIR
GRSRKLAELLRLNPKDGRLLYRPNKAGETPYNIDCSHQKSILTQIFGARHLSPTETD
GDMLGYDLYSSALADILSEPTMQPPICVGLYAQWGS GKSFLLKKLEDEMKTFA GQ
QIEPLFQFSWLIVFLTLLLCGGLGLLFAFTVHPNLGIAVSLSFLALLYIFFIVYFGGR
REGESWNWAWVLSTRLARHIGYLELLLLKLMFVNPPELPEQTTKALPVRFLFTDYN
10 RLSSVGGETSLAEMIATLSDACEREFGLATRLFRVFKTEDTQGKKKWKKTCCCLPS
FVIFLFIIGCIISGITLLAIFRVDPKHLTVNAV LISIASVVGLAFVLNCR TWQVLD SL
LNSQRKRLHNAASKLHKLKSEGFMKVLKCEVELMARMAKTIDSFTQNQTRLV VII
DGLDACEQDKVLQMLDTVRVLFSKGPFIAIFASDPHIIKAINQNLNSVLRDSNING
HDYMRNIVHLPVFLNSRGLSNARKFLVTSATNGDVPCSDTTGIQEDADRRVSQNS
15 LGEMTKLGSKTALNRRDTYRRRQMQR TITRQMSFDLTKLLVTEDWFSDISPQTMR
RLNIVSVTGRLLRANQISFNWDRLASWINLTEQWPYRTSWLILYLEETEGIPDQM
TLKTIYERISKNIPTTKDVEPLLEIDGDIRNFEVFLSSRTPVLVARDVKVFLPCTVNL
DPKLREIADVRAAREQISIGGLAYPPLPLHEGPPRAPSGYSQPPSVCSSTS FNGPFA
GGVVSPQPHSSYYSGMTGPQHFPYNRPFAPYLYTPRYYPGGSQHLSRPSVKTSL
20 PRDQNNGLEVIKEDAAEGLSSPTDSSRGSGPAPGPVLLNSLNVDAVCEK LKQIEG
LDQSM LPQYCTTIKKANINGRVLAQCNIDELKKEMNMNFGDWHLFRSTVLEM RN
AESHVVPEDPRFLSESSSGPAPHGEPARRASHNELPHTELSSQTPYTLNFSFEELNTL
GLDEGAPRHSNLSWQSQTRRTPSLSSLNSQDSSIEISKLTDKVQAEYRDAYREYIA
QMSQLEGGPGSTTISGRSSPHSTYYMGQSSSGGSIHSNLEQEKGKDSEPKPDDGRK
25 SFLMKRGDVIDYSSSGVSTNDASPLDPITEEDEKSDQSGSKLLPGKKSSERSSLFQT
DLKLKGSGLRYQKLPSDEDESGTEESDNTPLLKDDKDRKAEGKVERVPKSPEHSA
EPIRTFIKAKEYLSDALLDKKDSSDSGVRSSSESSPNHSLHNEVADDSQLEKANLIEL
EDDSHSGKRGIPHSLSGLQDPILARMSICSEDKKSPSECSLIASSPEENWPACQKAYN
LNRT PSTVT LNNNSAPANRANQN FDEMEGIRETSQVILRPSSSPNPTTIQ NENLKSM
30 THKRSQRSSYTRL SKDPPELHAAASSESTGFGEERESIL

MDLEGDRNGGAKKKNFFKLNNKSEKDKKEKKPTVSVFSMFYYSNWLDKLYMVV
GTLAAIIHGAGLPLMMLVFGEMTDIFANAGNLEDLMSNTNRSNDINDTGFFMNLEE
DMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMRQEIGWFD
VHDVGELNTRLTDDVSKINEGIGDKIGMFFQSMATFFTGFIVGFTRGWKLTIVILAI
5 SPVLGLSAAVWAKILSSFTDKELLAYAKAGAVAEVLAARTVIAFGGQKKELER
YNKNLEEAKRIGIKKAITANISIGAAFLLIYASYALAFWYGTTLVLSGEYSIGQVLT
VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGN
LEFRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGCGKSTTVQLMQRLYDP
TEGMVSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVTMDEIEKA
10 VKEANAYDFIMKLPKFDLTVGERGAQLSGGQKQRIAIARALVRNPKILLLDEATS
ALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAGFDDGVIVEKGNHDE
LMKEKGIYFKLVTMQTAGNEVELENAADESKSEIDALEMSSNDSRSSLIRKRSTRR
SVRGSQAQDRKLSTKEALDESIPPVSFWRIMKLNLTWPYFVVGVFCAIINGGLQP
AFAIIFSKIIGVFTRIDDPETKRQNSNLFSLFLALGIISFTTFFLQGFTFGKAGEILTKR
15 LRYMVFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAVITQNI
NLGTGIIISFTYGWQLTLLLLAIVPPIAAGVVEMKMLSGQALKDKKELEGAGKIATE
AIENFRTVVSLTQEQKFEHMYAQSLQVPYRNSLRKAHIFGITFSFTQAMMYFSYAG
CFRFGAYLVAHKLMSFEDVLLVFSAVVFGAMAVGQVSSFAPDYAKAKISAAHIIM
IIEKTPLIDSYSTEGLMPNTLEGNTFGEVVFNYPTRPDIPVLQGLSLEVKKGQTLA
20 LVGSSGCGKSTVVQLLERFYDPLAGKVLLDGKEIKRLNVQWLRAGHLGIVSQEPILF
DCSIAENIAYGDNSRVVSQEEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGG
QKQRIAIARALVRQPHILLLDEATSALDTESEKVVQEALDKAREGRTCIVIAHRLST
IQNADLIVVFQNGRVKEHGTHQQLLAQKGIYFSMVSQAGTKRQ

25 SEQ ID No: 19 (Neurotrypsin)

MTLARFVLALMLGALPEVVGFDVSLNDSLHSHRHSPAGPHYPPYLPTQQRPPR
TRPPPPLPRFPRPPRALPAQRPHALQAGHTPRPHPWGCPAGEPWVSVTDFGAPCLR
WAEVPPFLERSPPASWAQLRGQRHNFCSRPDGAGRPWCFYGDARGKVDWGYCD
CRHGSVRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGI
30 AKQTPFSGGLIPIYWSNVRRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCFSH
GPTFPIIRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAK
AWHQAYFGEGSGPVMLEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCTPL

TDGVIRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQ
ASANHFEESTGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGGE
GHRLSLGFPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYK
GPARARTMAYFGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
5 DYFGKKASGNSNKESSLSSVCGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSH
GDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEEFEEEEIGV
QQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQKTASNC
YITGWGDTGRAYSR TLQQA AIPLLPKRFCEERYKGRFTGRMLCAGNLHEHKRVDS
CQGDSSGGLMCERPGESWVVGVT SWGYGCGVKD SPGVYTKVSAFVPWIKSVT
10 KL

SEQ ID No: 20 (PLD3)

LA VVGFGALMTQLFLWEYGDLHLFGPNQRPAPCYDPCEAVLVESIPEGLDFPNAS
TGNPSTSQA WLGLLAGAHSSLDIASFYWTLTNNDTHTQEPSAQQGEEVLRQLQTL
15 APKGVNVRIA VSKPSGPQPQADLQALLQSGAQVRMVD MQKLTHGVLHTKFWV
DQTHFYLG SANMDWRSLTQVKELGVVMYNC SCLARDLT KIFEAYWFLGQAGSSI
PSTWPRFYDTRYNQETPMEICLNGTPALAYLASAPPPLCPSGRTPDLKALLNVVDN
ARSFYIVAVMNYLPTLEFSPHPRFWPAIDDGLRRATYERGVKVRLLISCWGHSEPS
MRAFLLSLAALRDNHTHSDIQVKLFVVPAD E AQARIPYARVNH NKYMVTERATYI
20 GTSNWSGNYFTETAGTSLLV TQNGRGGLRSQLEAIFLRDWDSPYSHDLDT SADS
V
GNACRLL

SEQ ID No: 21 (RetSDR2)

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKL
25 KSKLVLDINKHGLEETAACKCKGLGAKVHTFVVD CSNREDIYSSAKKVKA EIGD
VSILVNNAGVVYTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIV
TVASAAGHVSVPFLLAYCSSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNT
GFIKNPSTSLGPTLEPEEVVNRLMHGILTEQKMIFIPSSIAFLTTLERILPERFLAVLK
RKISVKFDAVIGYKMK AQ

30

SEQ ID No:22 (APLP2)

MAATGTAAAAATGRLLLLLVGLTAPALALAGYIEALAANAGTGFAVAEPQIAM
FCGKLNMHVNIQTGKWEPTGTGKSCFETKEEVLQYCQEMYPELQITNVMEANQ
RVSIDNWCRRDKKQCKSRFVTPFKCLVGEFVSDVLLVPEKCQFFHKERMEVCENH
QHWHTVVKEACLTQGMTLYSYGMLLPCGVDQFHGTEYVCCPQTKIIGSVSKEEEE
5 EDEEEEEEEDEEEDYDVYKSEFPTEADLEDFTEAAVDEDEDEEEEGEEVVEDRDY
YYDTFKGDDYNEENPTEPGSDGTMSDKEITHDVKA VCSQEAMTGPCRAVMPRW
YFDLSKGKCVRFYGGCGGNRNNFESEDYCMAVCKAMIPPTPLPTNDVDVYFETS
ADDNEHARFQKAKEQLEIRHRNRMDRVKKEWEEAELQAKNLPKAERQTLIQHFQ
AMVKALEKEAASEKQQLVETHLARVEAMLNDRRRMALENYLAALQSDPPRPHRI
10 LQALRRYVRAENKDRLHTIRHYQHVLAVDPEKAAQMKSQVMTHLHVIEERRNQS
LSLLYKVPYVAQEIQEIDEELLQEQRADMDQFTASISETPVDVRVSSEESIEPPFHP
FHPFPALPENEDTQPELYHPMKKSGVGEQDGLIGAEKVINSKNKVDENMVID
ETLDVKEMIFNAERVGGLEERESVGPLREDFSLSSSALIGLLVIAVAIATVIVISLV
MLRKRQYGTISHGIVEVDPMLTPEERHLNKMQNHGYENPTYKYLEQMQUI

15

SEQ ID No:23 (APP)

MLPGLALLLLAAWTARALEVPTDGNAGLLAEPQIAMFCGRLNMHMNVQNGKWD
SDPSGTTKCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHP
HFVIPYRCLVGEFVSDALLVPDKCKFLHQERMDVCETHLHWHTVAKETCSEKSTN
20 LHDYGMILLPCGIDKFRGVEFVCCPLAEESDNVDSADAEEDDSDVWWGGADTDY
ADGSEDKVVEVAEEEEVAEVEEEEADDEDDEDGDEVEEEAEOPYEEATERTTSI
ATTTTTTTESVEEVVREVCSEQAETGPCRAMISRWFYDVTEGKCAPFFYGGCGGN
RNNFDTEEYCMAVCGSAMSQSLLKTTQEPLARDPVKLPPTAASTPDAVDKYLETP
GDENEHAHFQKAKERLEAKHRERMSQVMREWEEAERQAKNLPKADKKA VIQHF
25 QEKVESLEQEAANERQQLVETHMARVEAMLNDRRRRLALENYTTALQAVPPRPH
VFNMLKKYVRAEQKDRQHTLKHFEHVRMVDPKKAAQIRSQVMTHLRVIYERMN
QSLSLLYNVPAVAEEIQDEVDPELLQKEQNYSDDVLANMISEPRISYGNDALMPSLT
ETKTTVELLPVNGEFSDDLQPWHSFGADSVANTENEVEPVDARPAADRGLTTR
PGSGLTNIKTEEISEVKMDAEFRHDSGYEVHHQKL VFFAEDVGSNKGAIIGLMVGG
30 VVIATVIVITLVMLKKKQYTSIHGVEVDAAVTPEERHLSKMQQNGYENPTYKF
FEQMQN

SEQ ID No: 24 (SXN1)

MSGELPPNINIKEPRWDQSTFIGRANHFFTVDPRNILLTNEQLESARKIVHDYRQG
IVPPGLTENELWRAKYTYDSAFHPDTGEKMILIGRMSAQVPMNMTITGCMMTFYR
TTPAVLFWQWINQSFNAVNYTNRSGDAPLTVNELGTAYVSATTGAVATALGLN
5 ALTKHVSPLIGRFVPFAAVAAANCINIPLMRQRELKVGIPVTDENG NRLGESANAA
KQAITQVVVSRILMAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCCLVF
ATPLCCALFPQKSSMSVTSLEAELQAKIQESHPELRRVYFNKGL

SEQ ID No: 25 (SORL1)

10 MATRSSRRESRLPFLFTLVALLPPGALCEVWTQRLHGGSAPLPQDRGFLVVQGD
RELRLWARGDARGASRADEKPLRRKRSAALQPEPIKVYGQVSLNDSHNQMVVH
WAGEKSNVIVALARDSLALARPKSSDVYVSYDYGKSFKKISDKLNFGLGNRSEAV
IAQFYHSPADNKRYIFADAYAQYLWITFDFCNTLQGFSPFRAADLLLHASKANLLL
GFD RSHPNKQLWKSDDFGQTWIMIQEHVKSFSWGIDPYDKPNTIYIERHEPSGYST
15 VFRSTDFQSRNQEVILEEVRDFQLRDKYMFATKVVHLLGSEQQSSVQLWVSFG
RKPMRAAQFVTRHPINEYYIADASEDQVFVCVSHSNRNTNLYISEAEGLKFSLSLE
NVLYYSPGGAGSDTLVRYFANEPPADFHRVEGLQGVYIATLINGSMNEENMRSVI
TFDKGGTWEFLQAPAFTGYGEKINCELSQGC SLHLAQRLS QLLNLQLRRMPILSKE
SAPGLIATGSVGKNLASKTNVYISSSAGARWREALPGPHYTTWGDHGGIITAIAQ
20 GMETNELKYSTNEGETWKTFFSEKPVFVYGLLTEPGEKSTVFTIFGSNKENVH
LILQVNATDALGVPCTENDYKLWSPSDERGNECLLGHKTVFKRRTPHATCFNGED
FDRPVVVSNCSC TREDYECDFGFKMSEDLSLEVCPDPEFSGKSYSPVPCPVGST
YRRTRGYRKISGDTCSGGDVEARLEGELVPCPLAEENEFILYAVRKSIIYRYDLASG
ATEQLPLTGLRAAVALDFDYEHNCLYWSDLALDVIQRLCLNGSTGQEVINS GLET
25 VEALAFEPLSQLLYWVDAGFKKIEVANPDGDFRLTIVNSSVLDRPRALVLPQEGV
MFWTDWGD LKPGIYRSNMDGSAA YHLVSEDVKWPNGISVDDQWIYWTDAYLEC
IERITFSGQQRSVILDNLPHYAIAVFKNEIYWDDWSQLSIFRASKYSGSQMEILAN
QLTGLMDMKIFYKGKNTGSNACVPRPCSLCLPKANNRSRSCRPEDVSSSVLP
DLMCDCPQGYQLKNNTCVKEENTCLRNQYRCSNGNCINSIWWCDFDND CGDMS
30 DERNCPPTICDLDTQFRCQESGTCIPLSYKCDLEDDCGDNSDESHCEMHQCRSDEY
NCSSGMCIRSSWVCDGDND CRDWSDEANCTAIYHTCEASN FQCRNGHCIPQRWA
CDGDTDCQDGSDEDPVNCEKKCNGFRCPNGTCIPSSKHCDGLRDCSDGSDEQHCE

PLCTHFMDFVCKNRQQCLFHSMVCDGIIQCRDGSDEDAAFAGCSQDPEFHKVCDDE
FGFQCQNGVCISLIWKCDGMDDCGDYSDEANCENPTEAPNCSRYFQFRCENGHCI
PNRWKCDRENDCGDWSDEKDCGDSHILPFSTPGPSTCLPNYYRCSSGTCVMDTW
VCDGYRDCADGSDEEACPLLANTAASTPTQLGRCDRFEFECHQPKTCIPNWKRC
5 DGHQDCQDGRDEANCPHSTLTCSREFQCEDGEACIVLSERCDGFLDCSDESDE
KACSELTVYKVQNLQWTADFSGDVTLTWMRPKKMPSASCVYNVYYRVVGESI
WKTLETHSNKTNTVLKVLKPDTTYQVKVQVQCLSKAHTNDFVTLRTPEGLPDA
PRNLQLSLPREAEGVIVGHWAPPIHTHGLIREYIVEYSRSGSKMWASQRAASNFTI
KNLLVNTLYTVRVA AVTSRGIGNWSDSKSITTKGKVIPPPDIHIDSYGENYLSFTLT
10 MESDIKVNNGYVVLFWAFDTHKQERRTLNFRGSILSHKVGNLTAHTSYEISAWAK
TDLGDSPLAFEHVMTRGVRPPAPSLKAKAINQTAVECTWTGPRNVVYGIFYATSF
LDLYRNPKSLTTSLHNKTVIVSKDEQYLFLVRVVVPYQGPSSDYVVVKMIPDSRLP
PRHLHVHTGKTSVVIKWESPYDSPDQDLYAIAVKDLIRKTDRSYKVKSRNSTV
EYTLNKLPGGKYHIVQLGNMSKDSSIKITTVSLSAPDALKIITENDHVLLFWKSL
15 ALKEKHFNESRGYEIHMFD SAMNTAYLGNTTDNFFKISNLKMGHNYTFTVQARC
LFGNQICGEPAILLYDELGSGADASATQAARSTDVA AVVPILFLILLSLGVGFAIL
YTKHRRLQSSFTAFANSHYSSRLGSAIFSSGDDLGEDDEDAPMITGFSDDVPMVIA

SEQ ID No: 26 (SPC18)

20 MLSLDFLDDVRRMNKRQLYYQVLNFGMIVSSALMIWKGLMVTGSESPIVVVLG
SMEPAFHRGDLLFLTNRVEDPIRVGEIVVFRIEGREIPVHRVLKIHEKQNGHIKFLT
KGDNNAVDDRGLYKQGQHWLEKKDVVGRARGFVPYIGIVTILMNDYPKFKYAV
LFLGLFVLVHRE

25 SEQ ID No: 27 (SPC22)

MNTVLSRANSLFAFSLSVMAALTFGCFITTA FKDRSVPVRLHVSRI MLKNVEDFTG
PRERSDLGFITSDITADLENIFDWNVKQLFLYLSAEYSTKNNALNQVVLWDKIVLR
GDNPKLLLKDMKTKYFFFDDGNGLKGNRNVTLTLSWNVVPNAGILPLVTGSGHV
SVPFPDTYEITKSY

30

SEQ ID No: 28 (SPC25)

MAAAAVQGGRSGGSGGCSGAGGASNCGTGSGRSGLLDKWKIDDKPKVKIDKWDG
SAVKNSLDDSAKKVLEKYKYVENFGLIDGRLTICTISCFFAIVALIWDYMHPPFES
KPVLAALCVISYPLFMLSFMGMILTIYTSYKEKSIFLVAHRKDPTGMDPDDIWQLS
SSLKRFDKDYTLKLTFISGRTKQQREAEFTKSIKFFDHSGTLVMDAYEPEISRLHD
5 SLAIERKIK

SEQ ID No: 29 (stearoyl-CoA desaturase)

MPAHLQDDISSYTTTTTITAPPSRVLQNGGDKLETMPLYLEDDIRPDIKDDIYDP
TYKDKEGPPSPKVEYVWRNIIIMSLHLGALYGITLIPTCKFYTWLWGVFYFVSAL
10 GITAGAHRLWSHRSYKARLPLRLFLIIANTMAFQNDVYEWARHDRAHHKFSETHA
DPHNSRRGFFFSHVGWLLVRKHPAVKEKGSTLDLSDLEAEKLVMFQRRYYKPGL
LMMCFILPTLVPWYFWGETFQNSVFVATFLRYAVVLNATWLVNAAHLFGYRPY
DKNISPRENILVSLGAVGEGFHNHYHHSFPYDYSASEYRWHINFITTFIDCMAALGL
AYDRKKVSKAAILARIKRTGDGNYKSG

15

SEQ ID No: 30 (TMP21)

MSGLSGPPARRGPFPLALLLFLGPRVLAISFHLPIINSRKCLREEIHKDLLVTGAY
EISDQSGGAGGLRSHLKITDSAGHILYSKEDATKGKFAFTTEDYDMFEVCFESKGT
GRIPDQLVILDMKHGVEAKNYEEIAKVEKLKPLEVELRRLEDLSEIVNDFAYMKK
20 REEEMRDTNESTNTRVLIFSIFSMFCLIGLATWQVFYLRFFKAKKLIE

SEQ ID No: 31 (VLCAD)

MSGCGLFLRTTAAARACRGLVVSTANRLLRTSPPVRAFAKELFLGKIKKKEVFPF
PEVSQDELNEINQFLGPVEKFFTEEVDNRKIDQEGKIPDETLEKLKSLGLFGLQVPEE
25 YGGLGFSNTMYSRLGEIISMDGSITVTLAAHQAIGLKGIIAGTEEQKAKYLPKLAS
GEHIAAFCLTEPASGSDAASIRSRTLSEDKKHYILNGSKVWITNGGLANIFTVFAK
TEVVDSDGSVKDKITAFIVERDFGGVTNGKPEDKLGIRGSNTCEVHFENTKIPVENI
LGEVGDGFKVAMNINLSGRFSMGSVVAGLLKRLIEMTAEYACTRKQFNKRLSEFG
LIQEKFALMAQKAYVMESMTYLTAGMLDQPGFDCSIEAAMVKVFSSEAAWQCVC
30 SEVLQILGGLGYTRDYPYERILRDTRILLIFEGTNEILRMYYALTGLQHAGRILTTRI
ELKQAKVSTVMDTVGRRLRDSLGRTVDLGLTGNHGVVHPSLADSANKFEENTYC
FGRTVETLLLRFGKTIMEEQLVLKRVANILINLYGMTAVLSRASRSIRIGLRNHDHE

VLLANTFCVEAYLQNLFSLSQLDKYAPENLDEQIKKVSQQILEKRAYICAHPLDRT
C

SEQ ID No: 32 (YMEIL1)

5 MFSLSSTVQPQVTVPLSHLINAFTPKNTSVSLSGVSVSQNQHRDVVPEHEAPSSSEF
SLNLRDLGLSELKIGQIDQLVENLLPGFCKGKNISSHWHTSHVSAQSFENKYGNL
DIFSTLRSSCLYRHHSRALQSICSDLQYWPVFIQSRGFKTLKSRTRRLQSTSERLAET
QNIAPSFVKGFLLRDRGSDVESLDKLMKTKNIPEAHQDAFKTGFAEGFLKAQALT
QKTNDSLRRLILFVLLFGIYGLLKNPFLSVRFRTTGLDSA VDPVQMKNVTFE
10 HVKGVVEEAKQELQEVVEFLKNPQKFTILGGKLPKGILLVGPPGTGKTLLARAVAG
EADVPFYYASGSEFDEMFGVGVGASRIRNLFREAKANAPCVIFIDELDSVGGKRIESP
MHPYSRQTINQLLAEMDGFKPNEGVIIGATNFPEALDNALIRPGRFDMQVTVPRP
DVKGRTEILKWYLNKIKFDQSVDEIARGTVGFSGAELENLVNQAALKA AVDGK
EMVTMKELEFSKDKILMGPERRSVEIDNKNKTITAYHESGHAILAYYTKDAMPINK
15 ATIMPRGPTLGHVSLLPENDRWNETRAQLLAQMDVSMGGRVAEELIFGTDHITTG
ASSDFDNATKIAKRMVTKFGMSEKLGVMYSDTGKLSPETQSAIEQEIRILLRDSY
ERAKHILKTHAKEHKNLAEALLTYETLDAKEIQIVLEGKKLEVR

SEQ ID No: 33 (LAPTM4B)

20 MVNYAWAGRSQRKLWWRSAVLTCKSVVRPGYRGGLQARRSTLLKTCARARA
TAPGAMKMVAPWTRFYNSNCCLCCHVRTGTILLGVWYLIINA VVLLILLSALADP
DQYNFSSSELGGDFEFMDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFC
YQIFDFALNMLVAITVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLILLFISIL
TFKGYLISCVWNCYRYINGRNSSDVLVYVTSNDTTVLPPYDDATVNGAAKEPPP
25 PYVSA

SEQ ID No: 34 (S100alpha)

MGSELETAMETLINVFHAHSGKEGDKYKLSKKELKELLQTELSGFLDAQKD VDA
VDKVMKELDENG DGEVDFQEYVVLVAALTVACNNFFWENS

30

SEQ ID No:35 (Cadherin EGF LAG seven-pass G-tpe receptor 2)

MRSPATGVPLPTPPPLLLLLLLLLLLLPPPLLGDQVGPCRSLSRGRGSSGACAPMGW
LCPSSASNLWLYTSRCDAGTELTGHLVPHHDGLRVWCPSESAHIPLPPAPEGCPW
SCRLLGIGGHLSPQGKLTLP EEHPCLKAPRLRCQSKLAQAPGLRAGERSPEESLG
GRRKRNVNTAPQFQPPSYQATVPENQPAGTPVASLRAIDPDEGEAGRLEYTMDAL
5 FDSRSNQFFSLDPVTGAVTTAEELDRETGSTHVFRVTAQDHGMPRRSALATLTILV
TDTNDHDPVFEQQEYKESLRENLEVGYEVLTVRATDGDAPPNANILYRLLEGSGG
SPSEVFEIDPRSGVIRTRGPVDREEVESYQLTVEASDQGRDPGRSTTA AVFLSVED
DNDNAPQFSEKRYVVQVREDVTPGAPVLRVTASDRDKGSNAV VHYSIMSGNARG
QFYLDAQTGALDVVSPLDYETTKEYTLRVRAQDGGRPPLSNVSGLVTVQVLDIND
10 NAPIFVSTPFQATVLESVPLGYLVLVHQAIDADAGDNARLEYRLAGVGHDFPFTIN
NGTGWISVAAELDREEVDFYSFGVEARDHGTPALTASASVSVTVLDVNDNNPTFT
QPEYTVRLNEDAAVGTSVVTVSAVDRDAH SVITYQITSGNTRNRFSITSQSGGGLV
SLALPLDYKLERQYVLAVTASDGTRQDTAQIVNVTDANTHRPVFQSSHYTVNV
NEDRPAGTTVVLISATDEDTGENARITYFMEDSIPQFRIDADTGAVTTQAELDYED
15 QVSYTLAITARDNGIPQKSDTTYLEILVNDVNDNAPQFLRDSYQGSVYEDVPPFTS
VLQISATDRDSGLNGRVFYTFQGGDDGDGDFIVESTSGIVRTLRLRDRENV AQYVL
RAYAVDKGMPPARTPMEVTVTVLDVNDNPPVFEQDEFDVFVEENSPIGLAVARVT
ATDPDEGTNAQIMYQIVEGNIPEVFQLDIFSGELTALVDLDYEDRPEYVLVIQATSA
PLVSRATVHVRLLDRNDNPPVLGNFEILFN NYVTNRSSSFPGGAIGRVPAHDPDISD
20 SLTYSFERGNELSLVLLNASTGELKLSRALDNNRPLEAIMSVLVSDGVH SVTAQCA
LRVTITDEMLTHSITLRL EDMSPERFLSPLLGLFIQAVAATLATPPDHVVVFNVQR
DTDAPGGHILNVSLSVGQPPGPGGGPPFLPSED LQERLYLNRSLT AISAQRVLPFD
DNICLREPCENYMRCVSVLRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGFTGDYC
ETEVDLCYSRPCGPHGRCRSREGGYTCLCRDGYTGEHCEVSARSGRCTPGVCKNG
25 GTCVNLLVGGFKCDCPSGDFEKP YCQVTTRSFP AHSFITFRGLRQRFHFTLALS FAT
KERDGLLLYNGRFNEKHDFVALEVIQE QVQLTFSAGESTTTVSPFVPGGVSDGQW
HTVQLKYYNKPLL GQTGLPQGPSEQKVAVVTVDGCDTGVALRFGSVLGNYS CA
QGTQGGSKKSLDLTGPLLGGVPDLPESFPVRMRQFVGCMRN LQVDSRHIDMA DF
IANNGTVPGCPAKKNVCDSNTCHNGGTCVNQWDAFSCECPLGFGGKSCAQEMAN
30 PQHFLGSSLVAWHGLSLPISQPWYLSLMFRTRQADGVLLQAITRGRSTITLQLREG
HVMLSVEGTGLQASSLRLEPGRANDGDWHHAQLALGASGGPGHAILSFDY GQQR
AEGNLGPRHLHLSNITVGGIPGPAGGVARGFRGCLQGVRVSDTPEGVNSLDPSH

GESINVEQGCSLPDPCDSNPCPANSYCSNDWDSYSCSCDPGYYGDNCTNVCDLNP
CEHQSVC TRKPSAPHGYTCECPPNYLGPYCETRIDQPCPRGWWGHPTCGPCNCDV
SKGFDPDCNKTSGECHCKENHYRPPGSPTCLLCDCYPTGSLSRVCDPEDGQCPCCKP
GVIGRQCDRCNDNPF AEVTTNGCEVNYDSCPRAIEAGIWWPRTRFGLPAAAPCPKG
5 SFGTAVRHCD EHRGWLPPNLFNCTSITFSELKGFAERLQRNESGLDSGRSQQ LALL
LRNATQHTAGYFGSDVKVAYQLATRLLAHESTQRGFGLSATQDVHFTENLLRVG
SALLDTANKRHWELIQQTEGGTAWLLQH YEAYASALAQNM RHTYLSPTTIVTPNI
VISVVRLDKGNFAGAKLPRYEALRGEQPPDLETTVILPESVFRET PPVVRPAGPGEA
QEPEELARRQRRHPELSQGEAVASVITYRTL AGLLPHNYDPDKRSLRVPKRPIINTP
10 VVSISVHDDEELLPRALDKPVTVQFRLLETEERTK PICVFWNHSILVSGTGGWSAR
GCEVVFRNESHVSCQCNHMTSFAVLMDVSRRENGEILPLKTLTYVALGVTLAALL
LTFFFLTLLRLRSNQHGIRRNLTAA LGLAQLVFL LGINQADLPFACTVIAILLHFLY
LCTFSWALLEALHLYRALTEVRDVNTGPMRFY YMLGWGVPAFITGLAVGLDPEG
YGNPDFCWL SIYDTLIWSFAGPVAF AVSMSVFLYIL AARASCAAQRQGF EKKGPV
15 SGLQPSFAVLLLLSATWLLALLSVNSDTLLFH YLFATCNCIQGPFIFLSYVVL SKEV
RKALKLACSRKPSDPALTTKSTLTSSYNCPSPYADGRLYQPYGDSAGSLHSTSRS
GKSQPSYIPFL REESALNPGQGPPGLGDPGSLFLEGQDQQHDPD TSDSDLSLEDD
QSGSYASTHSSDSEEEEEEEEEEEA AFPGEQGWDSLLGPGAERLPLHSTPKDGGPGP
GKAPWPGDFGTTAKESSGNGAPEERLRENGDALSREGSLGPLPGSSAQPHKGILKK
20 KCLPTISEKSSLLRLPLEQCTGSSRGSSASEGSRGGPPPRPPPRQSLQEQLNGVMPIA
MSIKAGTVDEDSSGSEFLFFNFLH

SEQ ID No:36 (Calsyntenin)

MLRRPAPALAPAARLLL AGLLCGGGVWAARVNKHK PWLEPTYHGIVTENDNTVL
25 LDPPLIALDKDAPLRFAESFEVTVTKEGEICGFKIHGQNV PFDAVVVDKSTGEGVIR
SKEKLDCELQKDYSFTIQAYDCGKGPDGTVNKKSHKATVHIQVNDVNEYAPVFK
EKSYKATVIEGKQYDSILRVEAVDADCSPQFSQICSYEITPDVPFTVDKDG YIKNTE
KLNYGKEHQYKLTVTAYDCGKKRATEDVLVKISIKPTCTPGWQGWN NRIEYEPG
TGALAVFPNIHLETCDEPVASVQATVELETSHIGKGCDRDTYSEKSLHRLCGAAAG
30 TAELLPSPSGSLNWTMGLPTDNGHDSQVFEFNGTQAVRIPDGVVSVPKEPFTIS
VWMRHGPFGRKKETILCSSDKTDMNRHHYSLYVHGCRLIFLFRQDPSEEKKYRPA
EFHWKLNQVCDEEWHHYVLNVEFPSVTLYVDGTSHEPFSVTEDYPLHPSKIETQL

VVGACWQEFSGVENDNETEPVTVASAGGDLHMTQFFRGNLAGLTLRSGKLADKK
VIDCLYTCKEGLDLQVLEDSEGRGVQIQAHPSQLVLTLEGEDLGELDKAMQHISYL
NSRQFPTPGIRRLKITSTIKCFNEATCISVPPVDGYVMVLQPEEPKISLSGVHHFARA
ASEFESSEGVFLFPELRIISTITREVEPEGDGAEDPTVQESLVSEEIVHDLDTCEVTVE
5 GEELNHEQESLEVDMARLQKKGIEVSSSELGMTFTGVDTMASYEEVLHLLRYRN
WHARSLDRKFKLICSELNGRYISNEFKVEVNVIIHTANPMEHANHMAAQPFVHP
EHRSFVDLSGHNLANPHPFVVPSTATVVIVVCVSFLVFMILGVFRIRAAHRRTM
RDQDTGKENEMDWDDSAITTVNPMETYEDQHSSEEEEEEEEEEESEDGEEEDDIT
SAESESSEEEEGEQGDPQNATRQQQLEWDDSTLSY

10

SEQ ID No: 37 (visinin-like 1)

MGKQNSKLAPVEMEDLVKSTEFNEHELKQWYKGFLKDCPSGRNLNLEEFQQLYVK
FFPYGDASKFAQHAFRTFDKNGDGTIDFREFICALSITSRGSFEQKLNWAFNMYDL
DGDGKTRVEMLEIEAIYKMVGTVIMMKMNEDGLTPEQRVDKIFSKMDKNKDD
15 QITLDEFKEAAKSDPSIVLLLQCDIQK

SEQ ID No: 38 (BACE1)

MAQALPWLLLWMGAGVLPAGHTQHGRILPLRSGLGGAFLGLRLPRETDEEPEEPG
RRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILDVTGSSNFAVGAAPHPFLH
20 RYYQRQLSSTYRDLRKG VYVPYTQGWEGELGTDLLCGAGFPLNQSEVLASVGG
SMIIGGIDHSLYTGSLWYTPIRREWYVEVIIVRVEINGQDLKMDCKEYNYDKSIVDS
GTTNLRPLPKKVFEAAVKSIIKAASTEKFPDGFVLGEQLVCWQAGTTPWNIFPVISL
YLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGF
YVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYNIPQTDESTLMT
25 IAYVMAAICALFMLPLCLMVCQWRCLRCLRQQHDDFADDISLLK

SEQ ID No: 39 (CELSR2)

MRSPATGVPLPTPPPPLLLLLLLLLPPPLLGDQVGPCRSLSRGRGSSGACAPMGW
LCPSSASNLWLYTSRCRDAGTELTGHLVPHHDGLRVWCPESEAHPLPPAPEGCP
30 WSCRLLGIGGHLSPQGKLTLP EEHPCLKAPRLRCQSCKLAQAPGLRAGERSPEESL
GGRRKRNVNTAPQFQPPSYQATVPENQAGTPVASLRAIDPDEGEAGRLEYTMDA
LFD SRSNQFFSLDPVTGAVTTAEELDRETKSTHVFRVTAQDHGMPPRRSALATLTIL

VTDTNDHDPVFEQQEYKESLRENLEVGYEVLTVRATDGDAPPNANILYRLLEGSG
GSPSEVFEIDPRSGVIRTRGPVDREEVESYQLTVEASDQGRDPGPRSTTAAVFLSVE
DDNDNAPQFSEKRYVVQVREDVTPGAPVLRVTASDRDKGSNAVHYSIMSGNAR
GQFYLDAQTGALDVVSPLDYETTKKEYTLRVRAQDGGRPPLSNVSGLVTVQVLDIN
5 DNAPIFVSTPFQATVLESVPLGYLVLVHQAIDADAGDNARLEYRLAGVGHDFPFTI
NNGTGWISVAAELDREEVDFYSFGVEARDHGTALASASVSVTVLDVNDNNPTF
TQPEYTVRLNEDAAVGTSVVTVSAVDRDAHSVTTYQITSGNTRNRFSTTSQSGGGL
VSLALPLDYKLERQYVLAVTASDGTRQDTAQIVNVNVDANTHRPVFQSSHYTVN
VNEDRPAGTTVVLISATDEDTGENARITYFMEDSIPQFRIDADTGA VTTQAELDYE
10 DQVSYTLAITARDNGIPQKSDTTYLEILVNDVNDNAPQFLRDSYQGSVYEDVPPFT
SVLQISATDRDSGLNGRVFYTFQGGDDGDGDFIVESTSGIVRTLRLDRENV AQYV
LRA YAVDKGMPPARTPMEVTVTVLDVNDNPPVFEQDEFDVFVEENSPIGLAVAR
VTATDPDEGTNAQIMYQIVEGNIPEVFQLDIFSGELTALVDLDYEDRPEYVLVIQAT
SAPLVSRATVHVRLLDRNDNPPVLGNFEILFN NYVTNRSSSFPGGAIGRVP AHD PDI
15 SDSLTYSFERGNELSLVLLNASTGELKLSRALDNNRPLEAIMSVLVSDGVHSVTAQ
CALRVTTITDEMLTHSITLRL EDMSPERFLSPLLGLFIQAVAATLATPPDHVVVFNV
QRDTDAPGGHILNVSLSVGQPPGPGGGPPFLPSEDLQERLYLNRSLT AIS AQRVLP
FDDNICLREPCENYMRCVSVLRFDSSAPFIASSSVLFRPIHPVGGLRCRCPPGFTGD
YCETEVDLCYSRPCGPHGRCSRREGGYTCLCRDGYTGEHCEVSARSGRCTPGVCK
20 NGGTCVNLLVGGFKCDCPSGDFEKP YCQVTT RSFP AHSFITFRGLRQRHFHTLALS
FATKERDGLLLYNGRFNEKHDFVALEVIQE QVQLTFSAGESTTTVSPFVPGGVSDG
QWHTVQLKYYNKPLLGTGLPQGPSEQKVA VVTVDGCDTGVALRFGSVLGNYS
CAAQGTQGGSKKSLDLTGPLLLGGVPDLPE SFPVRMRQFVGCMRNLQVDSRHID
MADFIANNGTVPGCPAKKNVCDSNTCHNGGTCVNQWDAFSCECPLGFGGKSCAQ
25 EMANPQHFLGSSLVAWHGLSLPISQPWYLSLMFRTRQADGVLLQAITRGRSTITLQ
LREGHVMLSVEGTGLQASSLRLEPGRANDGDWHHAQLALGASGGPGHAILSFDY
GQQRAEAGNLGPRLHGLHLSNITVGGIPG PAGGVARGFRGCLQGVRVSDTPEGVNS
LDPSHGESINVEQGC SLPDPCDSNPCPANSYCSNDWDSYSCSDPGYYGDNCTNV
CDLNPCEHQSVCTRKPSAPHGYTCECPPNYLGPYCETRIDQPCPRGWWGHPTCGP
30 CNCDVSKGFDPDCNKTSGECHCKENHYRPPGSPTCLLCD CYPTGSLSRVCDPEDG
QCCKPGVIGRQCDRCNPF AEVT TNGCEVNYDSCPRAIEAGIWWPRTRFGLPAA
APCPKGSFGTAVRHCDEHRGWLPPNLFNCT SITFSELKGFAERLQRNESGLDSGRS

QQLALLLRNATQHTAGYFGSDVKVAYQLATRLLAHESTQRGFGLSATQDVHFTE
NLLRVGSALLDTANKRHWELIQQTEGGTAWLLQHYEAYASALAQNMRYHTYLSPF
TIVTPNIVISVVRDLKGNFAGAKLPRYEALRGEQPPDLETTVILPESVFRETTPPVVRP
AGPGEAQEPEELARRQRRHPELSQGEAVASVIIYRTLGLLPHNYDPDKRSLRVPK
5 RPIINTPVVSISVHDDEELLPRALDKPVTVQFRLLTEERTKPICVFWNHSILVSGTG
GWSARGCEVVFRNESHVSCQCNHMTSFAVLMDVSRRENGEILPLKTLTYVALGV
TLAALLLTFFFLTLLRILRSNQHGIRRNLTAAALGLAQLVFLGGINQADLPFACTVIAI
LLHFLYLCTFSWALLEALHLYRALTEVRDVNTGPMRFYYMLGWGVPAFITGLAV
GLDPEGYGNPDFCWLSIYDTLIWSFAGPVAFVSMVFLYLAARASCAAQRQGF
10 EKKGPVSGLQPSFAVLLLLSATWLLALLSVNSDTLLFHLYFATCNCIQGPFIFLSYV
VLSKEVRKALKLACSRKPSDPALTSTLTSSYNCPSPYADGRLYQPYGDSAGSL
HSTSRSGKSQPSYIPFLLREESALNPGQGPPGLGDPGSLFLEGQDQQHDPDTSDDSD
LSLEDDQSGSYASTHSSDSEEEEEEEEEEEAAFPGEQGWDSLLGPGAERLPLHSTPK
DGGPGPGKAPWPGDFGTAKESSGNGAPEERLRENGDALSREGSLGPLPGSSAQP
15 HKGILKKKCLPTISEKSSLLRPLEQCTGSSRGSSASEGSRGGPPPPRPPRQSLQEQL
NGVMPIAMSIKAGTVDEDSSGSEFLFFNFLH

SEQ ID No: 40 (FADS2)

MGKGGNQGEAAEREVSVPFWSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHP
20 GGQRVIGHYAGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKIT
EDFRALRKTAEDMNLFKTNHVFFLLLLAHIALESIAWFTVIFYFGNGWIPTLITAFV
LATSQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLK GASANWWNHRHFQ
HHAKPNIFHKDPDVNMLHVFLGEWQPIEYGKKKLKYL PYNHQHEYFFLIGPPLLI
PMYFQYQIIMTMIVHKNWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRFLESH
25 WFWVVTQMNHIVMEIDQEA YRDWFSSQLTATCNVEQSFFNDWFSGHLNFQIEHH
LFPTMPRHNLHKIAPLVKSLCAKHGIEYQEKPLL RALLDIIRSLKKSGLWLDAYL
HK

SEQ ID No: 41 (NogoA)

30 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLER
TEFSELEYSEMGSFSVSPKAESA VIVANPREEII VKNKDEEEKLVSNILHNQQELP
TALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKE

DS DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDR
SGAYITCAPFNPAATESIATNIFLLGDPTSENKTDEKKIEBKKAQIVTEKNTSTKTS
NPFLVAAQDSETDYVTTDNLT KVTEE VVANMPEGLTPDLVQEACESELNEVTGK
IA YETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPS
5 AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENIN
AALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPD
SEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMIEYENKEKLSALPPEGGKP
YLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDL FISKEAQIRE
TETFS DSSPIEIDEFTL LISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL
10 PHDSLKNIQPKVEEKISFSDDFS KN GSATSKVLLLPPDVSALATQAEIESIVKPKVL
VKEAEKKLPDTEKEDRSPSAIFSABL SKTSVVDLLYWRDIKKTGVVFGASLFLLS
LTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQ
KYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILA
LISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE

15

SEQ ID No: 42 (OS-9)

MAAETLLSLLGLLLLGLLLPASLTGGVGS LNLEELSEMRYGIEILPLVVMGGQSQS
SDVVIVSSKYKQRYECRLPAGAIHFQREREETPAYQGPGIPELLSPMRDAPCLLKT
KDWWTYEF CYGRHIQQYH MEDSEIKGEVL YLGYYQSAFDWDETA KASKQHRL
20 KRYHSQTYGNGSKCDLNGRPREAEVRFLCDEGAGISGDYIDRVDEPLSCSYVLTIR
TPRLCPHPLL RP PPSAAPQAILCHPSLQPEEYMA YVQRQAVDSKQYGDKIEELQDL
GPQVWSETKSGVAPQKMAGASPTKDDSKDSDFWKMLNEPEDQAPGGEEVPAEE
QDPSPEAADSASGAPNDFQNNVQVKVIRSPADLIRFIEELKGGTKKGKPNIGQEQP
VDDAAEVPQREPEKERGDPERQREMEEEDEDEDEDEDEDERQLLGEFEKELEGIL
25 LPSDRDLRLRSEVKAGMEREL ENIIQEAS PALPPT EKELDPDGLKKESERDRAMLAL
TSTLNKLIKRL EEKQSP ELVKKHKKKR VVPKKPPSPQPT EEDPEHRVRVRVTCLR
LG GPNQDLTVLEMKREN PQLKQIEGLVKELLEREG LTAAGKIEIKIVRPWAE GTEE
GARWLTDEDTRNLKEIFFNILVPGAEEAQKERQRQKELESNYRRVWGSPGGEGTG
DLDEFDF

30

SEQ ID No: 43 (PDGFRB)

MRLPGAMPALALKGELLLLLLLLLLEPQISQGLVVTTPGPELVLVNSSTFVLTCGS
APVVWERMSQEPPQEMAKAQDGTFSVLTLNLTLGLDTGEYFCTHNSRGLTDE
RKRLYIFVPDPTVGFLPNDAEELFIFLTEITEITIPCRVTDLPQLVVTLHEKKGDVALP
VPYDHQRGFGIFEDRSYICKTTIGDREVDSDAYYVYRLQVSSINVSNAVQTVVR
5 QGENITLMCIVIGNEVVNFETYPRKEVIGRLVEPVTDFLDMPYHIRSILHPSAEL
EDSGTYTCNVTESVNDHQDEKAINITVVESGYVRLLEGEVGTLLQFAELHRSRTLQV
VFEAYPPPTVLWFKDNRTLGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGH
YTMRAFHEDAEVQLSFQLQINVPVRVLELSESHPDSSGEQTVRCRGRGMPQPNIIWS
ACRDLKRCPRELPPTLLGNSSEEEESQLETNVTYWEEEQEFVVSTLRLQHVDRLPS
10 VRCTLRNAVGGDTQEVIVVPHSLPFKVVVISAILALVVLTIISLILIMLWQKKPRYE
IRWKVIESVSSDGHEYTYVDPMQLPYDSTWELPRDQLVLGRTLGSAGFGQVVEAT
AHGLSHSQATMKVAVKMLKSTARSSKQALMSELKIMSHLGPLNVVNLLGACT
KGGPIYITEYCRYGDLVDYLHRNKHTFLQHHSKRRPPSAELYSNALPVGLPLPS
HVSLTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVPS
15 APERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICE
GKLVKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILL
WEIFTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRP
PFSQLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPLDTSS
VLYTAVQPNEGDNDYIPLPDPKPEVADEGLEGSPSLASSTLNEVNTSSTISCDSP
20 EPQDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAEDSFL

SEQ ID No: 44 (PTK7)

MGAARGSPARPRRLPLLSVLLLPLGGTQTAIVFIKQPSSQDALQGRRALLRCEVE
APGPVHVYWLLDGAPVQDTERFAQGSSLSFAAVDRLQDSGTFQCVARDDVTGE
25 EARSANASFNKWIEAGPVVLKHPASEAEIQPQTQVTLRCHIDGHPRTYQWFRDG
TPLSDGQSNHTVSSKERNLTLRPAGPEHSGLYSCCAHSAGQACSSQNFTLSIADES
FARVVLAPQDVVVARYEEAMFHCQFSAQPPPSLQWLFEDETPTITNRSRPPHLRRAT
VFANGSLLLTQVRPRNAGIYRCIGQGQRGPPILEATLHLAEIEDMPLFEPRVFTAGS
EERVTCCLPPKGLPEPSVWWEHAGVRLPTHGRVYQKGHELVLANIAESDAGVYTC
30 HAANLAGQRRQDVNITVATVPSWLKKPQDSQLEEGKPGYLDCLTQATPKPTVVW
YRNQMLISEDSRFEVFKNGTLRINSVEVYDGTWYRCMSSTPAGSIEAQRVQVLE
KLKFTPPPQPQQCMEFDKEATVPCSATGREKPTIKWERADGSSLPEWVTDNAGTL

HFARVTRDDAGNYTCIASNGPQGQIRAHVQLTVAVFITFKVEPERTTVYQGHTAL
LQCEAQGDPKPLIQWKGKDRILDPTKLGPRMHIFQNGSLVIHDVAPEDSGRYTCIA
GNSCNIKHTEAPLYVVDKPVPEESEGPGSPPPYKMIQTIGLSVGAAVAYIIAVLGLM
FYCKKRCKAKRLQKQPEGEEPEMECLNGGPLQNGQPSAEIQEEVALTSLGSGPAA
5 TNKRHSTSDKMHFPRSSLQPITTLGKSEFGEVFLAKAQGLEEGVAETLVLVKSLQS
KDEQQQLDFRRELEMFGLNHNANVVRLLGLCREAPHYMVLEYVDLGLDKQFLR
ISKSKDEKLKSQPLSTKQKVALCTQVALGMEHLSNNRFVHKDLAARNCLVSAQR
QVKVSALGLSKDVYNSEYYHFRQAWVPLRWMSPEAILEGDFSTKSDVWAFGVL
MWEVFTHGEMPHGGQADDEVLADLQAGKARLPQPEGCPSKLYRLMQRCWALSP
10 KDRPSFSEIASALGDSTVDSKP

SEQ ID No: 45 (UGCGL1)

MGCKGDASGACAAGALPVTGVCYKMGVLVVLTVLWLFSSVKADSKAITTSLTTK
WFSTPLLEASEFLAEDSQEKFWNFVEASQNIGSSDHDGTDYSYYHAILEAAFQFL
15 SPLQQNLFKFCLSLRSYSATIQAQQIAADEPPPEGCNSFFSVHGKKTCESDTLEAL
LLTASERP KPLLFGDHRYPSSNPESPVVIFYSEIGSEEF SNFHRQLISKSNAGKINY
VFRHYIFNPRKEPVYLSGYGVELAIKSTEYKAKDDTQVKGTEVNTTVIGENDPIDE
VQGFLFGKLRDLHPDLEGQLKELRKHLVESTNEMAPLKVWQLQDLSFQTAARILA
SPVELALVVMKDLSQNFPTKARAITKTAVSSEL RTEVEENQKYFKGTGLQPGDS
20 ALFINGLHMDLDTQDIFSLFDVLRNEARVMEGLHRLGIEGLSLHNVLKLNIPSEA
DYAVDIRSPAISWVNNLEVDSRYNSWPSSLQELLRPTFPGVIRQIRKNLHNMVFIV
DPAHETTAELMNTAEMFLSNHIPLRIGFIFVNDSEVDGMQDAGVAVLRAYNVYV
AQEVDDYHAFQTLTHIYNKVRTGEKVKVEHVSVLEKKYPYVEVNSILGIDSAID
RNRKEARGYYEQTG VGPLPVVLFNGMPFEREQ LDPDELETTMHKILETTTFFQRA
25 VYLGELPHDQDVVEYIMNQPNVVRINSRILTAERDYLDLTASNFFVDDYARFTI
LDSQGKTAAVANSMNYLTKKGMSSKEIYDDSFIRPVTFWIVGDFDSPSGRQLLYD
AIKHQKSSNNVRISMINNPAKEISYENTQISRAIWAALQTQTSNAAKNFTTKMAKE
GAAEALAAGADIAEFSVGGMDFSLFKEVFESSKMDFILSHAVYCRDVLKLLKKGQR
AVISNGRIIGPLEDSELFNQDDFHLLNIIKLTSGQKIKSHIQQLRVEEDVASDLVMK
30 VDALLSAQPKGDPRIEYQFFEDRHS AIKLRPKEGETYFDVVA VVDPVTREARLAP
LLL VLAQLINMNLRFVMNCQSKLSDMPLKSFYRYVLEPEISFTSDNSFAKGPIAKFL
DMPQSPLFTLNLNTPESWMVESVRTPYDLDNITYLEEVD SVVAAEYELEYLLLEGH

CYDITTGQPPRGLQFTLGTSANPVIIVDTIVMANLGYFQLKANPGAWILRLRKGRSE
DIYRIYSHDGTDSPPDADEVVIVLNNFKSKIIVKVQKKADMVNEDLLSDGTSENE
SGFWDSFKWGFTGQKTEEVKQDKDDIINFVSGHLYERFLRIMMLSVLKNTKTP
VKFWFLKNYLSPTFKEFIPYMANEYNFQYELVQYKWPRWLHQQTEKQRIIWGYKI
5 LFLDVLFPPLVVDKFLFVDADQIVRTDLKELRDFNLDGAPYGYTPFCDSRREMDGY
RFWKSGYWASHLAGRKYHISALYVVDLKKFRKIAAGDRLRGQYQGLSQDPNSLS
NLDQDLNPNMIHQVPIKSLPQEWLWCETWCDDASKKRAKTIDLCNNPMTKEPKL
EAAVRIVPEWQDYDQEIQLQIRFQKEKETGALYKEKTKEPSREGPQKREEL

10 SEQ ID No: 46 (CtnnB1)

MATQADLMELDMAMEPDRKAAVSHWQQQSYLDSGIHSGATTTAPSLSGKGNPEE
EDVDTSQVLYEWEQGFSSQSTQEQQVADIDGQYAMTRAQVRAMFPETLDEGM
QIPSTQFDAAHPTNVQRLAEPSSQMLKHA VVNLYNQDDAELATRAIPELTKLLNDE
DQVVVNKAAVMVHQLSKKEASRHAIMRSPQMVSIVRTMQNTNDVETARCTAG
15 TLHNLSHHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLLHQEGAKMA
VRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLILASGGPQALVNIM
RTYTYEKLWTTSRVLKVLSSCNKPAIVEAGGMQALGLHLDPSQRLVQNCL
WTLRNLSDAATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTCNNYKNKM
MVCQVGGIEALVRTVLRAGDREDITEPAICALRHLSRHQEAEMAQNAVRLHYGL
20 PVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDT
QRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNIRIVIRGLNTIPLFVQLL
YSPIENIQRVAAGVLCELAQDKAEAEAEAGATAPLTELHLSRNEGVATYAAAVL
FRMSDKPQDYKKRLSVELTSSLFRTEPMAWNETADLGLDIGAQGEPLGYRQDDP
SYRSFHSGGYGQDALGMDPMEHEMGGHHPGADYPVDGLPDLGHAQDLMDGL
25 PPGDSNQLAWFDTDL

SEQ ID No: 47 (CtnnA1)

MTAVHAGNINFKWDPKSLEIRTLAVERLLEPLVTQVTTLVNTNSKGPSNKKRGRS
KKAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKAAAG
30 EFADDPCSSVKRGNMVRAAPALLSAVTRLLILADMADVYKLLVQLKVVEDGILKL
RNAGNEQDLGNQYKALKPEVDKLNMAAKRQQELKDVGHRDQMAAARGILQSN
VPILYASQACLQHPDVAA YKANRDLIYKQLQQA VTGISNAAQATASDDASQHQ

GGGGGELAYALNNFDKQIIVDPLSFSEERFRPSLEERLESIIISGAALMADSSCTRDD
RRERIVAECNAVRQACRTCSEYMGNA GRKERSDALNSAIDKMTKKTRDLRRQL
RKAVMDHVSDSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLA
CSISNNEEGVKLVRMSASQLEAGCPQVINAATWALAPKPQSKLAQENMDLFKEQ
5 WEKQVRVLTDAVDDITSIDDFLA VSENHILEDVNKCVIALQEKDVGDLDRTAGAI
RGRAARVIHVVTSEMDNYEPGVYTEKVLEATKLLSNTVMPRFTEQVEAAVEALSS
DPAQPMDENEFIDASRLVYD GIRDIRKAVLMIRTPEELDDSD FETEDFDVRSETSVQ
TEDDQLIAGQSARAIMAQLPQEQKAKIREQVASFQEEKSKLDAEVSKWDDSGNDII
VLAKQCMCMIMMEMTDFTRGKGPLKNTSDVISAACKIAEAGSRMDKLGRTIRDHC
10 PDSACKQDLLAYLQRIALYCHQLNICKSVKAEVQNLGGELVVSNGCDTCGALQGL
KGWPPPLCLATHWVDSAMSLIQA AKNLMNAV VQTVKASYVASTKYQKSQGMAS
LNLPAVSMKMKAPKPLVKREKQDETQTKIKRASQKKHVNPVQALSEFKAMDS
I

15 SEQ ID No: 48 (CtnnA2)
MTSATSPIILKWDPKSLEIRTLTVERLLEPLVTQVTTLVNTSNKGPSGKKKGRSKKA
HVLAASVEQATQNFLEKGEQIAKESQDLKEELVAAVEDVRKQGETMRIASSEFAD
DPCSSVKRGTMVRAARALLSAVTRLLILADMADVMRLLSHLKIVEEAEAVKNAT
NEQDLANRFKEFGKKMVKLNYVAARRQQELKDPHCRDEMAAARGALKKNATM
20 LYTASQAFLRHPDVAATRANRDYVFKQVQEAIAGISNAAQATSPTDEAKGHTGIG
ELAAALNEFDNKIILDPMTFSEARFRPSLEERLESIIISGAALMADSSCTRDDRRERIV
AECNAVRQALQDLLSEYMNNTGRKEKGDPLNIAIDKMTKKTRDLRRQLRKAVM
DHISDSFLETNVPLLVLIEAAKSGNEKEVKEYAQVFREHANKLVEVANLAC SISNN
EEGVKLVRMAATQIDSLCPQVINAALTLAARPQSKVAQDNMDVFKDQWEKQVR
25 VLTEAVDDITSVDDFLSVSENHILEDVNKCVIALQEGDVDTLDRTAGAIRGRAARV
IHIINAEMENYEAGVYTEKVLEATKLLSETVMPRFAEQVEVAIEALSANVPQPFEE
NEFIDASRLVYDGVVRDIRKAVLMIRTPEELEDSDFEQEDYDVRRGTSVQTEDDQL
IAGQSARAIMAQLPQEEKAKIAEQVEIFHQEKS KLDAEVAKWDDSGNDIIVLAKQ
MCMIMMEMTDFTRGKGPLKNTSDVINAACKIAEAGSRMDKLARAVADQCPDSA
30 CKQDLLAYLQRIALYCHQLNICKSVKAEVQNLGGELIVSGTG VQSTFTTFYEVD CD
VIDGGRASQLSTHLPTCAEGAPIGSGSSDSSMLDSATSLIQA AKNLMNAVVLTVKA

SYVASTKYQKVYGTAAVNSPVVSWKMKAPEKKPLVKREKPEEFQTRVRRGSQK
KHISPVQALSEFKAMDSF

SEQ ID No: 49 (CtnnD1)

5 MDDSEVESTASILASVKEQEAQFEKLTRALEEERRHVSAQLERVRVSPQDANPLM
ANGTLTRRHQNGRFVGDADLERQKFSDLKLNGPQDHSLLYSTIPRMQEPGQIVE
TYTEEDPEGAMSVVSVETSDDGTTTRRTETTVKKVVKTVTTRTVQPVAMGPDGLP
VDASSVSNNYIQTIGRDFRKNNGGGPGPYVGQAGTATLPRNFHYPPDGYSRHYE
DGYPGGSNDYGSLSRVTRIEERYRPSMEGYRAPSQRQDVYGPQPQVRVGGSSVDLH
10 RFHPEPYGLEDDQRSMGYDDLDYGMMSDYGTARRTGTPSDPRRRLRSYEDMIGE
EVPSDQYYWAPLAQHERGSLASLDSLKGGPPPPNWRQPELPEVIAMLGFRLLDAV
KSNAAYLQHLCYRNDKVKTDVRKLKGIPVLVGLLDHPKKEVHLGACGALKNIS
FGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGTLWNLSSHDSIKMEIVD
HALHALTDEVIIPHSGWEREPNEDCKPRHIEWESVLTNTAGCLRNVSSERSEARRK
15 LRECDGLVDALIFIVQAEIGQKSDSKLVENCVCLLRNLSYQVHREIPQAERYQEA
APNVANNTGPHAASCFGAKKGKGGKPIEDPANDTVDFPKRTSPARGYELLFQPEV
VRIYISLLKESKTPAILEASAGAIQNLCAGRWTYGRYIRSALRQEKALSAIADLLTN
EHERVVKAASGALRNLAVDARNKELIGKHAIPNLVKNLPGGQQNSSWNFSEDTVI
SILNTINEVIAENLEAAKKLRETQGIEKLVLINKSGNRSEKEVRAAALVLQTIWGYK
20 ELRKPLEKEGWKKSDQVNLNNASRSQSSHSYDDSTLPLIDRNQKSDKKPDREEIQ
MSNMGSNTKSLDNNYSTPNERGDHNRITLDRSGDLGDMELKGTTPLMQDEGQES
LEEELDVLVLDDEGGQVSYPMSQKI

SEQ ID No: 50 (NCadh)

25 MCRIAGALRTLLPLLLALLQASVEASGEIALCKTGFPEDVYSAVLSKDVHEGQPLL
NVKFSNCNGKRKVQYESSPADFKVDEDGMVYAVRSFPLSSEHAKFLIYAQDKET
QEKWQVAVKLSLKPTLTEESVKESAEVEEIVFPRQFSKHSGLHQRQKRDWVIPPIN
LPENSRGFPFQELVRIRSDRDKNLSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLD
REQIARFHLRAHAVDINGNQVENPIDIVINVIDMNDNRPEFLHQVWNGTVPEGSKP
30 GTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTPSPNMFTINNETGDIITVAAGLD
REKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTDVNDNPPEFTAMTFYGEVPEN
RVDIIVANLTVTDKQPHTPAWNAVYRISGGDPTGRFAIQTDPNNSNDGLVTVVKPI

DFETNRMFVLTVA AENQVPLAKGIQHPPQSTATVSVTVIDVNENPYFAPNPKIIRQ
EEGLHAGTMLTTFTAQDPDRYMQQNIRYTKLSDPANWLKIDPVNGQITTI AVLDR
ESPNVKNNIYNATFLASDNGIPPMSGTGTLQIYLLDINDNAPQVLPQEAETCETPDP
NSINITALDYDIDPNAGPFAFDLPLSPVTIKRNWTTITRLNGDFAQLNLKIKFLEAGIY
5 EVPIITDSGNPPKSNISILRVKVCQCDSDNGDCTDVDRIVGAGLGTGAIIALLCIIILLI
LVLMFVVWMKRRDKERQAKQLLIDPEDDVDRDNILKYDEEGGGEEDQDYDLSQLQ
QPDTVEPDAIKPVGIRRM DERPIHAEPQYPVRS AAPHPGDIGDFINEGLKAADNDPT
APPYDSLLVFDYEGSGSTAGSLSSLNSSSSSGGEQDYDYLDNDWGPRFKKLADMYGG
GDD

10

SEQ ID No:51 (Reelin)

MERSGWARQTFLALLLGATLRARAAAGYYPRFSPFFFLCTHHGELEGDGEQGEV
LISLHIAGNPTYYPVGQ EYHVTISTSTFFDGLLVTGLYTSTSVQASQSIGGSSAFGFG
IMSDHQFGNQFMCSVVASHVSHLPTTNLSFTWIAPPAGTGCVNFMATATHRGQVIF
15 KDALAQQLCEQGAPTDVTVPHLA EIHS DSILRDDFDSYHQLQLNPNIWVECNNC
ETGEQCGAIMHGNAVTFCEPYGPRELITTGLNTTTASVLQFSIGSGSCRFSYS DPSII
VLYAKNNSADWIQLEKIRAPSNVSTIIHILYLPEDAKGENVQFQWKQENLRVGEVY
EACWALDNILIINSAHRQVVLEDSDLPVDTGNWLFPGATVKHSCQSDGNSIYFHG
NEGSEFN FATTRD VDLSTEDIQEQWSEEFESQPTGWDVLGAVIGTECGTIESGLSM
20 VFLKDGERKLCTPSMDTTGYGNLRFYFVMGGICDPGN SHENDIILYAKIEGRKEHI
TLDTLSYSSYKVP SLVSVINPELQTPATKFCLRQKNHQGHNRNVWAVDFFHVLP
VLPSTM SHMIQFSINL GCGTHQPGNSVSLEFSTNHGRSWSLLHTECLPEICAGPHLP
HSTVYSSENYSGWNRITIPNAALTRNTRIRWRQTGPILGNMW AIDNVYIGPSCL
KFCSGRGQCTR HGCKCDPGFSGPACEMASQTFPMFISESFGSSRLSSYHNFYSIRGA
25 EVSFGCGVLASGKALVFNKEGRRQLITSFLDSSQSRFLQFTLRLGSKSVLSTCRAPD
QPGEGVLLHYSDNGITWKLLEHYSYLSYHEPRIISVELPGDAKQFGIQFRWWQPY
HSSQREDVWAIDEIIMTSVLFNSISLDFTNLVEVTQSLGFYLG NVQPYCGHDWTLC
FTGDSKLASSMR YVETQSMQIGASYMIQFSLVMGCGQKYTPHMDNQVKLEYSTN
HGLTWHLVQEECLPSMPSCQEFTSASIYHASEFTQWRRVIVLLPQKTWSSATRFR
30 WSQSYYYTAQDEWALDSIYIGQQCPNMCSGHGSCDHGICRCDQGYQGTECHPEAA
LPSTIMSDFENQNGWESDWQE VIGGEIVKPEQCGVISSGSSLYFSKAGKRQLVSW
DLDTSWVDFVQFYIQIGGESASCNKPD SREEGVLLQYSNNGGIQWHLLAEMYFSD

FSKPRFVYLELPAAAKTPCTRFRWWQPVFSGEDYDQWAVDDIHLSEKQKQIIPVIN
PTLPQNFYEKPAFDYPMNQMSVWMLANEGMVKNETFCAATPSAMIFGKSDGDR
FAVTRDLTLKPGYVLQFKLNIGCANQFSSTAPVLLQYSHDAGMSWFLVKEGCYPA
SAGKGCEGNSRELSEPTMYHTGDFEEWTRITIVIPRSLASSKTRFRWIQESSSQKNV
5 PPFGLDGVYISEPCPSYCSGHGDCISGVCFCDLGYTAAQGTCSNVPNHNEMFDRF
EGKLSPLWYKITGAQVGTGCGTLNDGKSLYFNGPGKREARTVPLDTRNIRLVQFYI
QIGSKTSGITCIKPRTRNEGLIVQYSNDNGILWHLLRELD FMSFLEPQIISIDL PQDAK
TPATAFRWWQPQH GKHS AQWALDDVLIGMNDSSQTGFQDKFDGSIDLQANWYRI
QGGQVDIDCLSM D TALIFTENIGKPRYAETWDFHVSASTFLQFEMSMGCSKPFSNS
10 HSVQLQYSLNNGKDWHLVTEECVPPTIGCLHYTESSIYTSERFQNWKRITVYLPLS
TISPRTRFRWIQANYTVGADSWAIDNVVLASGCPWMCSGRGICDAGRCVCDRGFG
GPYCVPVVPLPSILKDDFNGNLHPDLWPEVYGAERGNLNGETIKSGTSLIFKGEGL
RMLISRDLDCTNTMYVQFSLRFI AKSTPERSHSILLQFSISGGITWHLMDEFYFPQT
NILFINVPLPYTAQT NATRFLWQPYNNGKKEEIWIVDDFIIDGNNVNNPVMLLDT
15 FDFGPREDNWWFFYPGGNIGLYCPYSSKGAPEEDSAMV FVSNEVGEHSITTRDLNVN
ENTIIQFEINVGCSTDSSSADPVRLEFSRDFGATWHLLLPLCYHSSSHVSSLCSTEHH
PSSTYYAGTMQGWRRREV VHFGLHL CGSVRFRWYQGFYPAGSQPVTW AIDNVYI
GPQCEEMCNGQGSCINGTKCICDPGYSGPTCKISTKNPDLKDDFEGQLES DRFL
MSGGKPSRKCGILSSGNNLFFNEDGLRMLMTRDLDLSHARFVQFFMRLGCGKGVP
20 DPRSQPVLLQYSLNGGLSWSLLQEFLFSNSSNVGRYIALEIPLKARSGSTRLRWWQ
PSENGHFYSPWVIDQILIGGNISGNTVLEDDFTTLD SRKWLLHPGGTKMPVCGSTG
DALVFIEKA STRYVSTDVAVNEDSFLQIDFAASC SVTDSCYAIELEYSVDLGLSW
HPLVRDCLPTNVECSR YHLQRILVSDTFNKWTRITLPLPPYTRSQA TRFRWHQPAP
FDKQQTW AIDNVYIGDGCIDMCSGHGRCIQGNCVCDEQWGGLYCDDPETS LPTQ
25 LKDNFNRAPSSQNWLTVNGGKLSTVCGAVASGMALHFSGGCSRLLVTVDLNLTN
AEFIQFYFMYGCLITPNNRNQGV LLEYSVNGGITWNLLMEIFYDQYSKPGFVNILL
PPDAKELATRFRWWQPRHDGLDQNDWAIDNV LISGSADQRTVMLD TFSSAPVPQH
ERSPADAGPVGRIAFDMFMEDKTSVNEHWLFHDDCTVERFCDSPDGVM LCGSHD
GREVYAVTHDLTPTEGWIMQFKISVGCKVSEKIAQNQIHVQYSTDFGVSWNYLVP
30 QCLPADPKCSGSVSQPSVFFPTKGWK RITYPLPESLVGNPVRF RFYQKYSMDMQWAI
DNFYLGPGCLDNCRGHGDCLREQCICDPGYSGPNCYLTHTLKTF LKERFDSEEIKP
DLWMSLEGGSTCTECGILAE D TALYFGGSTVRQAVTQDLDLRGAKFLQYWGRIGS

ENNMTSCHRPICRKEGVLLDYSTDGGITWTLHEMDYQKYISVRHDYILLPEDALT
NTTRLRWQPFVISNGIVVSGVERAQWALDNILIGGAEGINPSQLVDTFDDEGTSHE
ENWSFYFNAVRTAGFCGNPSFHLYWPNKKKDKTHNALSSRELIIQPGYMMQFKIV
VGCEATSCGDLHSVMLEYTKDARSDSWQLVQTQCLPSSSNSIGCSPFQFHEATTYN
5 SVNSSSWKRITIQLPDHVSSSATQFRWIQKGEETEKQSWAIDHVYIGEACPKLCSG
HGYCTTGAICICDESFQGDDCSVFSHDLPSYIKDNFESARVTEANWETIQGGVIGSG
CGQLAPYAHGDSL YFNGCQIRQAATKPLDLTRASKIMFVLQIGSMSQTDSCNSDLS
GPHAVDKAVLLQYSVNNGITWHVIAQHQP KDFTQAQRVSYNVPLEARMKGVLLR
WWQPRHNGTGHDQWALDHVEVVLVSTRKQNYMMNFSRQHGLRHFYNRRRRSL
10 RRY P

SEQ ID No:52 (Sortilin-related receptor)

MATRSSRRESRLPFLFTLVALLPPGALCEVWTQRLHGGSAPLPQDRGFLVVQGDP
RELRLWARGDARGASRADEKPLRRKRSAAALQPEPIKVYGQVSLNDSHNQMVVH
15 WAGEKSNVIVALARDSLALARP KSSDVYVS YDYGKSFKKISDKLNFGLGNRSEAV
IAQFYHSPADNKRYIFADAYA QYLWITFDFCNTLQGFSPFRAADLLLHASKANLLL
GFDRSHPNKQLWKSDDFGQ TWIMIQEHVKSFSWGIDPYDKPNTIYIERHEPSGYST
VFRSTDFQ SRENQE VILEEVRDFQLRDKYMFATKV VHLLGSEQQSSVQLWVSFG
RKPMRAAQFVTRHPINEYYIADASEDQVFVCVSHSNNRTNLYISEA EGLKFSLSLE
20 NVLYYSPGGAGSDTLVR YFANEFPADFHRVEGLQGVYIATLINGS MNENMRSVI
TFDKGGTWEFLQAPAF TGYGEKINCELSQGCSLHLAQRLS QLLNLQLRRMPILSKE
SAPGLIATGSVGKNLASKTNVYISSAGARWREALPGPHYTTWGDHGGIITAI AQ
GMETNELKYSTNEGETWKTFIFSEKPVFVYGLL TEPGEKSTVFTIFGSNKENVHSW
LILQVNATDALGV PCTENDYKLWSPS DERGNECLLGHKT VFKRRTPHATCFNGED
25 FDRPVVVSNC SCTREDECDFGFKMSEDLSLEV CVPDPEFSGKSYSPVP CPVGST
YRRTRGYRKISGDTCSGGDVEARLEGELVPCPLAEENEFILYAVRKSIYRYDLASG
ATEQLPLTGLRAAVALDFDYEHNCLYWSDLALDVIQRLCLNGSTGQEVINS GLET
VEALAFEPLS QLLYWVDAGFKKIEVANPDGDFRLTTVNSSVLDRPRALVLVPQEGV
MFWTDWGD LKPGIYRSNMDGSAA YHLVSEDVKWPNGISVDDQWYWTDAYLEC
30 IERITFSGQQRSVILDNLPHPYAIAVFKNEIYWDDWSQLSIFRASKYSGSQMEILAN
QLTGLMDMKIFYKGKNTGSNACVPRPCSLCLPKANNRSRSCRPEDVSSSVLP SG
DLMCDCPQGYQLKNNTCVKEENTCLRNQYRCSNGNCINSIWWCDFDND CGDMS

DERNCPTTICDLDTQFRCQESGTCIPLSYKCDLEDDCGDNSDESHCEMHQCRSDEY
NCSSGMCIRSSWVCDGDNDCRDWSDEANCTAIYHTCEASNFQCRNGHCIPQRWA
CDGDTDCQDGSDEDPVNCEKKCNCFRCPNGTCIPSSKHCDGLRDCSDGSDEQHCE
PLCTHFMDFVCKNRQQCLFHSMVCDGIIQCRDGSDEDAAFAGCSQDPEFHKVCDE
5 FGFQCQNGVCISLIWKCDGMDDCGDYSDEANCENPTEAPNCSRYPQFRCENGHCI
PNRWKCDREND CGDWSDEKDCGDSHILPFSTPGPSTCLPNYYRCSSGTCVMDTW
VCDGYRDCADGSDEEACPLL ANVTAASTPTQLGRCDRFEFECHQPKTCIPNWKRC
DGHQDCQDGRDEANCPTHSTLTCMSREFQCEDGEACIVLSERCDGFLDCSDESDE
KACSDELTVYKVQNLQWTADFSGDVTLTWMRPKKMPSASC VYNVYYRVVGESI
10 WKTLETHSNKTNTVLKVLKPDTTYQVKVQVQCLSKAHNTNDFVTLRTPEGLPDA
PRNLQLSLPREAEGVIVGHWAPPIHTHGLIREYTV EYSRSGSKMWASQRAASNFT EI
KNLLVNTLYTVRVA AVTSRGIGNWSDSKSITTIGKVIPPD IHDSYGENYLSFTLT
MESDIKVNGYVVNLFWAFDTHKQERRTLNFRGSILSHKVG NLT AHTSYEISAWAK
TDLGDSPLAFEHVMTRGVRPPAPSLKAKAINQTA VECTWTGPRNVVYGIFYATSF
15 LDLYRNP KSLTTS LHNKT VIVSKDEQYLFLVRVVVPYQGPSSDYVVVKMIPDSRLP
PRHLHVHTGKTSVVIK WESPYDSPDQDLLYAI AVKDLIRKTDRSYKVKS RNSTV
EYTLN KLEPGGKYHIIVQLGNMSKDSSIKITTVSLSAPDALKIITENDHVLLFWKSL
ALKEKHFNESRGY EIHMFDSAMNTAYLGNTTDNFFKISNLKMGHNYTFTVQARC
LFGNQICGEPAILLYDELGSGADASATQAARSTDVAA VVVPILFLILLSLGVGFAIL
20 YTKHRR LQSSFTAFANSHYSSRLGSAIFSSGDDLGEDDEDAPMITGFSDDVPMVIA

SEQ ID No:53 (18 kDa microsomal signal peptidase subunit)

MLSLDFLDDVRRMNRQLYYQVLNFGMIVSSALMIWKGLMVTGSESPIVVVL SG
SMEPAFHRGDLLFLTNRVEDPIRVGEIVVFRIEGREIPVHRVLKIHEKQNGHIKFLT
25 KGDNNAVDDRGLYKQGQHWLEKKDVVGRARGFVPYIGIVTILMNDYPKFKYAV
LFLGLFVLVHRE

SEQ ID No: 54 (CLGN)

HLPKQQRGGVCLGVKSKWQPKLRTGREKINMHFQAFWLCLGLLFISINAEFMDD
30 DVETEDFEENSEEIDVNESELSSEIKYKTPQPIGEVYFAETFD SGRLAGWVLSKAKK
DDMDEEISIIDGRWEIEELKENQVPGDRGLVLKSRAKHHAISAVLAKPFIFADKPLI
VQYEVNFQDGDICGGAYIKLLADTDDLILENFYDKTSYIIMFGPDKCGEDYKLHFIF

RHKHPKTGVFEEKHAKPPDVLDKKFFTDKRKTHLYTLVMNPDDTFEVLVDQTVVN
KGSLLLEDVVPPIKPPKEIEDPNDDKKPEEWDERAKIPDPSAVKPEDWDESEPAQIEDS
SVVKPAGWLDDEPKFIPDPNAEKPDDWNEDTDGEWEAPQILNPACRIGCGEWKPP
MIDNPKYKGVWRPPLVDNPNYQGIWSPRKIPNPDYFEDDHPFLLTSFSALGLELWS
5 MTSDIYFDNFICSEKEVADHWAADGWRWKIMIANANKPGVLKQLMAAAEGHP
WLWLIYLVTAGVPIALITSFCWPRKVKKKHKDTEYKKT DICIPQTKGVLEQEEKEE
KAALEKPMDL EEEKKQNDGEMLEKEEESEPEEKSEEEIEIEGQEE SNQSNKSGSED
EMKEADESTGSGDGPIKSVRKRRVRKD

10 SEQ ID No:55 (ECSIT)

MSWVQATLLARGLCRAWGGTCGAALTGTSISQVPRRLPRGLHCSAAAHSSSEQSL
VPSPPEPRQRPTKALVPFEDLFGQAPGGERDKASFLQTVQKFAEHSVRKRGHIDFTY
LALRKMREYGVERDLAVYNQLLNIFPKFVFRPRNIIQRIFVHYPRQQECGIAVLEQ
MENHGVMPNKETEFLLIQIFGRKSYPMKLKVLRLKLWFRFMNVNPFVPRDLPQD
15 PVELAMFGLRHMEPDLSARVTIYQVPLPKDSTGAADPPQPHIVGIQSPDQQAALAR
HNPAPVVFVEGPFSLWLRNKC VYYHILRADLLPPEEREVEETPEEWNLYYPMQLD
LEYVRSGWDNYEFDINEVEEGPVFAMCMAGAHDQATMAKWIQGLQETNPTLAQI
PVVFRLAGSTRELQTSSAGLEEPPLPEDHQEEDDNLQRQQQGGQS

20 SEQ ID No:56 (FLJ20342)

MPSASCDTLLDDIEDIVSQEDSKPQDRHFVRKDVVPKVRRRNTQKYLQEEENSPPS
DSTIPGIQKIWIRTWGCSHNNSDGEYMAQGLAA YGYKITENASDADLWLLNSCTV
KNPAEDHFRNSIKKAQEENKKIVLAGCVPQAQPRQDYLKGLSIIGVQQIDRVVEV
EETIKGHSVRLLGQKKDNGRRLGGARLDLPKIRKNPLIEIISISTGCLNACTYCKTK
25 HARGNLASYPIDELVDRAKQSFQEGVCEIWLTS EDTGAYGRDIGTNLPTLLWKL
EVIPEGAMLRLGMTNPPYILEHLEEMAKILNHPRVYAFLHIPVQSASDSVLMEMKR
EYCVADFKRVVDLKEKVPGITIATDIICGFPGETDQDFQETVKLVEEYKFPSLFIN
QFYPRPGTPAAKMEQVPAQVKKQRTKDLSRVFHSYSPYDHKIGERQQVLVTEESF
DSKFYVAHNQFYEQVLVPKNPAFMGKMVEVDIYESGKHFMKGQPVSDAKVYTPS
30 ISKPLAKGEVSGLT KDFRNGLGNQLSSGSHTSAASQCDSASSRMVLPMPRLHQDC
ALRMSVGLALLGLLFAFFVKVYN

SEQ ID No:57 (KIAA0090)

MAAEWASRFLWATLLIPAAAVYEDQVGKFDWRQQYVGKVKFASLEFSPGSKK
LVVATEKNVIAALNSRTGEILWRHVDKGTAEGAVDAMLLHGQDVITVSNGGRIM
RSWETNIGGLNWEITLDSGSFQALGLVGLQESVR YIAVLKKTTLALHHLSSGHLK
5 WVEHLPESDSIHYQM VYSYSGSVVWALGVVPFSHV NIVKFNVEDGEIVQQVRVS
TPWLQHLSGACGVVDEAVLVCPDPSSRSLQTLALETEWELRQIPLQSLDLEFGSGF
QPRVLPTQPNPVDASRAQFFLHLSPSHYALLQYHYGTL SLLKNFPQTALVSFATTG
EKTVAAVMACRNEVQKSSSSEDGSMGSFSEKSSSKDSLACFNQTYTINLYLVETG
RRLLDTTTTFSLEQSGTRPERLYIQVFLKKDDSVGYRALVQTEDHLLLFLQQLAGK
10 VVLWSREESLAEVVCLEMVDLPLTGAQAELEGEFGKKADGLLGMFLKRLSSQLIL
LQAWTSHLWKMFYDARKPRSQIKNEINIDTLARDEFNLQKMMVMVTASGKLFGI
ESSSGTILWKQYLPNVKPDSSFKLMVQRTTAHFPHPPQCTLLVKDKESGMSSLYVF
NPIFGKWSQVAPPVLKRPILQSLLLPVMQDYAKVLLLIDDEYKVTAFPATRNVLR
QLHELAPSIFFYLVD AEQGRLCGYRLRKDLTTELSWELTIPPEVQRIVKVKGKR SSE
15 HVHSQGRVMGDRSVLYKSLNPNLLAVVTESTDAHHERTFIGIFLIDGVTGRIIHSSV
QKKAKGPVHIVHSENWVVYQYWNTKARRNEFTVLELYEGTEQYNATAFSSSLDRP
QLPQVLQQSYIFPSSISAMEATTITERGITSRHLLIGLPSGAILSLPKALLDPRRPEIPTE
QSREENLIPYSPDVQIHAERFINYNQTVSRMRGIYTAPSGLESTCLVVAYGLDIYQT
RVYPSKQFDVLKDDYDYVLISSVLFGLVFATMITKRLAQVKLLNRAWR

20

SEQ ID No:58 (NICE-3)

MASGSNWLSGVNVVLVMA YGSLVFVLLFIFVKRQIMRFAMKSRRGPHVPVGHNA
PKDLKEEIDIRLSRVQDIKYEPQLLADDDARLLQLETQGNQSCYNYLYRMKALDAI
RTSEIPFHSEGRHPRSLMGKNFRSYLLDLRNTSTPFKGVRKALIDTLDDGYETARY
25 GTGVFGQNEYLRYQEALSELATAVKARIGSSQRHHQSAAKDLTQSPEVSPTTIQVT
YLPSSQKSKRAKH FLELKSFKDN YNTLESTL

SEQ ID No: 59 (CK2B)

MSSSEEVSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILD
30 LEPDEELEDNPNQSDLIEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPR
VYCENQPMPLIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTGFPH
MLFMVHPEYRPKRPANQFVPRLYGFKIHPMAYQLQLQAASNFKSPVKTIR

SEQ ID No: 60 (PTP LOC114971)

MAATALLEAGLARVLFYPTLLYTLFRGKVPGRAHRDWYHRIDPTVLLGALPLRSL
TRQLVQDENVRGVITMNEEYETRFLCNSSQEWKRLGVEQLRLSTVDMTGPTLDN
5 LQKGVQFALKYQSLGQCVYVHCKAGRSRSATMVAAYLIQVHKWSPEEAVRAIAK
IRSYHIRPGQLDVLKEFHKQITARATKDGTFFVISK

SEQ ID No: 61 (STT3)

MTKFGFLRLSYEKQDTLLKLLILSMAAVLSFSTRLFAVLRFESVIHEFDPYFNYRTT
10 RFLAEEGFYKFHNWFDDRAWYPLGRIIGGTIYPGLMITSAAIYHVLHFFHITIDIRN
VCVFLAPLFSSFTTIVTYHLTKELKDAGAGLLAAAMIAVVPGYISRSVAGSYDNEG
IAIFCMLLTYYMWIKAVKTGSICWAAKCALAYFYMVSSWGGYVFLINLIPLHVLV
LMLTGRFSHRIYVAYCTVYCLGTILSMQISFVGFQPVLSSEHMAAFGVFGLCQIHA
FVDYLRSKLNPPQFEVLFRSVISLVGVFLLTVGALLMLTGKISPWTGRFYSLDPS
15 YAKNNIPIIASVSEHQPTTWSSYYFDLQLLVFMFPVGLYYCFSNLSDARIFIMYGV
TSMYFSAVMVRLMLVLAPVMCILSGIGVSQVLSTYMKNLDIRPDKKSKKQDST
YPIKNEVASGMILVMAFFLITYTFHSTWVTSEAYSSPSIVLSARGGDGSRIIFDDFRE
AYYWLRHNTPEDAKVMSWWDYGYQITAMANRTILVDNNTWNNTHISRVGQAM
ASTEELKAYEIMRELDVSYVLVIFGGLTGYSSDDINKFLWMVRIGGSTDTGKHIKEN
20 DYYTPTGEFRVDREGSPVLLNCLMYKMCYYRFGQVYTEAKRPPGFDRVRNAEIG
NKDFELDVLEEA YTTEHWLVRIYKVKDLNDRGLSRT

SEQ ID No: 62 (NicAChRa3)

MGSGPLSLPLALSPPRLLLLLLLLSLLPVARASEAEHRLFERLFEDYNEIRPVANVSD
25 PVIIHFEVSMSQLVKVDEVNQIMETNLWLKQIWNDYKLKWNPSDYGGAEFMRVP
AQKIWKPDIVLYNNAVGDFQVDDKTKALLKYTG EVTWIPPAIFKSSCKIDVTYFPF
DYQNCTMKFGSWSYDKAKIDLVLIGSSMNLKDYWESGEWAIIKAPGYKHDIKYN
CCEEIYPDITYSLYIRRLPLFYTNLIIPCLLISFLTIVL VFYLPSDCGEKTLCISVLLSL
TVFLLVITETIPSTSLVIPLIGEYLLFTMIFVTL SIVITVFVLNVHYRTPTTHTMPSWV
30 KTVFLNLLPRVMFMTRPTSNEGNAQKPRPLYGAELSNLNCFSRAESKGCKEGYPC
QDGMCGYCHHRIKISNFSANLTRSSSSSESVDVLSLSALSPEIKEAIQSVKYIAEN
MKAQNEAKEEQKAQEIQQLKRKEKSTETSDQEPGL

SEQ ID No: 63 (SLC4A2)

MSSAPRRPAKGADSFCTPEPESLGP GTPGFPEQEDELHRTLGV FEEILQEAGSR
GGEEPGRSYGEEDFEYHRQSSHHHHPLSTHLPPDARRRKTPQGPGRKPRRRPGAS
5 PTGETPTIEEGEEDEDEASEAEGARALTQPSVSTPSSVQFFLREDD SADRKAERTS
PSSPAPLPHQEATPRASKGAQAGTQVEEAEAEAVAVASGTAGGDDGGASGRPLPK
AQPGHRSYNLQERRRIGSMTGAEQALLPRVPTDEIEAQT LATADLDLMKSHRFED
VPGVRRHLVRKNAKGSTQSGREGREPGTPRARPRAPHKPHEVFVELNELLLDKN
QEPQWRETARWIKFEEDVEEETERWGKPHVASLSFRSLLELRRTLAHGAVLLDLD
10 QQTLPGVAHQVVEQMVISDQIKAEDRANVLRALLLKHSHPSDEKDFSFRNISAGS
LGSLLGHHHGQGAESDPHVTEPLMGGVPETRLVERERDVPPPAPPAGITRSKSKH
ELKLEKIPENAEATVVLVGCVEFLSRPTMAFVRLREAVELDAVLEVPVPVRFLFL
LLGPSSANMDYHEIGRSISTLMSDKQFHEAAYLADEREDLLTAINAFLDCSVVLPP
SEVQGEELLRSVAHFQRQMLKKREEQGRLLPTGAGLEPKSAQDKALLQMVEAAG
15 AAEDDPLRRTGRPFGLIRDVRRRYPHYLSDFRDALDPQCLAAVIFYFAALSPAIT
FGGILLGEKTQDLIGVSELMSTALQGVVFCLLGAQPLL VIGFSGPLLVFEEAFFSFC
SNHLEYLVGRVWIGFWLVFLALLMVALEGSFLVRFVSRFTQEIFAFLISLIYETFY
KLVKIFQEHLHGCSASNSSEVDGGENMTWAGARPTLGPGNRSLAGQSGQGKPR
GQPNTALLSLVLMAGTFFIAFFLRKFKNRFFPGRIRRVIGDFGVPIAILIMVLVDYS
20 IEDTYTQKLSVPSGFSVTAPEKRGWVINPLGEKSPFPVWMMVASLLPAILVFILIFM
ETQITTLISKKERMLQKSGGFHLDLLIVAMGGICALFGLPWLAAATVRSVTHAN
ALTVMASKAVAPGDKPKIQEVKEQRTVGLLVALLVGLSIVIGDLLRQIPLAVLFGIFL
YMGVTSNLNGIQFYERLHLLLMPPKHHPDVTYVKKVRTLRMHLFTALQLLCLALL
WAVMSTAASLAFPFILITVPLRMVVLTRIFTDREM KCLDANAEFPVDEREGVDE
25 YNEMPMPV

SEQ ID No: 64 (HIFPH3/EGLN3)

MKGKGNQGEAAEREVSVP TFSWEEIQKHNLRTDRWLVIDRKVYNTKWSIQHP
GGQRVIGHYAGEDATDAFRAHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKIT
30 EDFRALRKTAEDMNLFKTNHVFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFV
LATSAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGASANWWNHRHFQ
HHAKNIFHKDPDVNMLHVFLGEWQPIEYGKKKLKYL PYNHQHEYFFLIGPPLLI

PMYFQYQIIMTMIVHKNWVDLAWAVSYIRFFITYIPFYGILGALLFLNFIRFLESH
WFWVVTQMNHIVMEIDQEAYRDWFSSQLTATCNVEQSFFNDWFSGHLNFQIEHH
LFPTMPRHNHKKIAPLVKSLCAKHGIEYQEKPLLRALLDIIRSLKKSGLWLDAYL
HK

5

SEQ ID No:65 (STX10)

MSLEDPPFFVVRGEVQKAVNTARGLYQRWCELLQESAAVGREELDWTNENRNL
RSIEWDLEDLEETIGIVEANPGKFKLPAGDLQERKVFVERMREAVQEMKDHMVSP
TAVAFLENNREILAGKPAAQKSPDLLDASAVSATSRYIEEQATQQLIMDEQDQ
10 QLEMVSGSIQVLKHMSGRVGEELDEQGIMLDFAQEMDHTQSRMDGVLRKLAK
VSHMTSDRRQWCAIAVLVGVLLLVLILLFSL

SEQ ID No:66 (Presenilin-2)

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEED
15 GEEDPDRYVCSGVPGRPPGLEEELTLKYGAKHVIMLFVPVTLCMIVVVATIKSVRF
YTEKNGQLIYTPFTEDTPSVGQRLNSVLNTLIMISVIVVMTIFLVVLYKYRCYKFI
HGWLIMSSMLLFLFTYIYLGEVLKTYNVAMDYPTLLLTVWNFGAVGMVCIHWK
GPLVLQQAYLIMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRML
VETAQERNEPIFPALYSSAMVWTVGMAKLDPSSQGALQLPYDPEMEEDSYDSFG
20 EPSYPEVFEPPLTGYPGEELEEEERGVKLGLGDFIFYSVLVGKAAATGSGDWNTT
LACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQL
YI

SEQ ID No:67 (Wolframin)

MDSNTAPLGPSCPQPPAPQPQARSRLNATASLEQERSERPRAPGPQAGPGPGVRD
25 AAAPAEPPQAQHTRSRRERADGTGPTKGDMEIPFEEVLERAKAGDPKAQTEVGKHY
LQLAGDTDEELNSCTAVDWLVLAQKGRREAVKLLRRCLADRRGITSENEREVR
QLSSETDLERA VRKAALVMYWKLNPKKKKQVAVAELENVGVNEHDGGAQPG
PVPKSLQKQRRMLERLVSSSESKNYIALDDFVEITKKYAKGVIPSSLFLQDDEDDDE
30 LAGKSPEDLPLRLKVVKYPLHAIMEIKEYLIDMASRAGMHWLSTIIPTHHINALIFF
FIISNLTIDFFAFFIPLVIFYLSFISMVICTLKVFQDSKAWENFRTLTDLLLRFEPNLDV
EQAEVNFNGWNHLEPYAHFLLSVFFVIFSFPISKDCIPCSELA VITGFFT VTSYLSLS

THAEPYTRRALATEVTAGLLSLLPSMPLNWPYLKVLGQTFITVPVGHLLVVLNVSV
PCLLYVYLLYLFFRMAQLRNFKGTICYLVPYLVCFMWCELSVVILLESTGLGLLR
ASIGYFLFLFALPILVAGLALVGVLQFARWFTSLELTKIAVTVAVCSVPLLLRWWT
KASFSVVGMMVKSLTRSSMVKLILVWLTAIVLFCWFYVYRSEGMMKVYNSTLTWQQ
5 YGALCGPRAWKETNMARTQILCSHLEGHRVTWTGRFKYVRVTDIDNSAESAINM
LPFFIGDWMRCLYGEAYPACSPGNTSTAEEELCRLKLLAKHPCHIKKFDRYKFEIT
VGMPFSSGADGSREREEDDVTKDIVLRASSEFKSVLLSLRQGSLEFSTILEGRLGSK
WPVFELKAISCLNCMAQLSPTRRHVKIEHDWRSTVHGAVKFAFDFFFFPFLSAA

10 SEQ ID No:68 (BACE1)

MAQALPWLLLWMGAGVLPAGHTQHGIRLPLRSGLGGAAPLGLRLPRETDEEPEEPG
RRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILDVTGSSNFAVGAAPHPFLH
RYYQRQLSSTYRDLRKGVYVPYTQGWEGELGTDLVSIHPGNVTVRANIAAITE
SDKFFINGSNWEGLGLAYAEIARPDDSLPFFDSL VKQTHVPNLFSLQLCGAGFPL
15 NQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDK
KEYNYDKSIVDSGTTNLRPKKVFEAAVKSIIKAASTEKFPDGFVLGEQLVCWQA
GTPWNIFPVISLYLMGEVTNQSFRTILPQQYLRPVEDVATSQDDCYKFAISQSST
GTVMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCG
YNIPQTDESTLMTIAYVMAAICALFMLPLCLMVCQWRCLRLRQHQHDFADDISL
20 LK

SEQ ID No:69 (FLJ30668)

MELHYLAKKSNQADLCDARDWSSRGLPGDQADTAATRAALCCQKQCASTPRAT
EMEGSKLSSSPASPSSSLQNSTLQPDAPFPGLLHSGNNQITAERKVCNCCSQELET
25 FTYVDKNINLEQRNRSSPSAKGHNHPGELGWENPNNEWSQEAASLISEEEDDTSSE
ATSSGKSIDYGFISAILFLVTGILLVIISYIVPREVTVDPNNTVAAREMERLEKESARLG
AHLDRCVIAGLCLLTGGVILSCLLMMSMWKGELYRRNRFASSKESAKLYGSFNF
RMKTSTNENTLELSLVEEDALAVQS

30 SEQ ID No:70 (BSCv protein)

MSEADGLRQRRPLRPQVVTDDDGAPEAKDGSSFSGRVFRVTFLMLAVSLTVPLL
GAMMILLESPIDPQPLSFKEPPLLLGVLPNTKLRQAERLFENQLVGPESIAHIGDVM

FTGTADGRVVKLENGEIETIARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADA
YKGLFEVNPWKREVKLLLSSETPIEGKNMSFVNDLTVTQDGRKIYFTDSSSKWQR
RDYLLLVMEGTDDGRLLEYDTVTREVKVLLDQLRFPNGVQLSPAEDFVLVAETT
MARIRRVYVSGLMKGGADLFVENMPGFDPNIRPSSSGGYWVGMSTIRPNPGFSML
5 DFLSERPWIKRMIFKLFSQETVMKFVPRYSLVLELSDSGAFRRSLHDPDGLVATYIS
EVHEHDGHL YLGSFRSPFLCRLSLQAV

SEQ ID No:71 (FLJ39249)

MAPRPLGPLVLALGGAAAVLGSVLFILWKTYFGRGRERRWDRGEAWWGAEAAAR
10 LPEWDEWDPEDEEDEEPALEEEQREVLVLGLDGAGKSTFLRVLSGKPPLEGHIPT
WGFNSVRLPTKDFEVDLLEIGGSQNLRFYWKEFVSEVDVLVFVVD SADRLRLPWA
RQELHKLLDKDPDLPVVVVANKQDLSEAMSMGELQRELGLQAIDNQREVFLAA
SIAPAGPTFEETPGTVHIWKLLLELLS

15 SEQ ID No:72 (Cgl-13)

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELII
FEILGVLNSSSRYPYFWKMNLCVILLILVFMVPPFYIGYFIVSNIRLLHKQRLLFSCLLW
LTFMYFFWKLGDPPILSPKHGILSIEQLISR VGVIGVTLMALLSGFGAVNCPYTYM
SYFLRNVTDTDILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFW
20 GMIKSVTTSASGSENLTLIQQEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKY
FNFLGYFFSIYCVWKIFMATINIVFDRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHI
SFILVGIIIVTSIRGLLITLTKFFYAISSSKSSNVIVLLLAQIMGMYFVSSVLLIRMSMP
LEYRTITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

25 SEQ ID No:73 (ITCH)

MSDSGSQLGSMGSLTMKSQIQITVISAKLKENKKNWFGPSPYVEVTVDGQSKKTE
KCNNTNSPKWKQPLTVIVTPVSKLHFRVWSHQTLKSDVLLGTAALDIYETLKSNN
MKLEEVVVTLQLGGDKPTETIGDLSICLDGLQLESEVVTNGETTCSENGVSCLCP
RLECNSAISAHCNLCPLGSDSPISASRVAGFTGASQNDGSRSKDETRVSTNGSD
30 DPEDAGAGENRRVSGNNSPSLSNGGFKPSRPPRPSRPPPTPRRPASVNGSPSATSE
SDGSSTGSLPPTNTNTNTSEGATSGLIPLTISGGSGPRPLNPVTQAPLPPGWEQRVD
QHGRVYYVDHVEKRTTWDRPEPLPPGWERRVDNMGRIYYVDHFTRTTTWQRPT

LESVRNYEQWQLQRSQLQGAMQQFNQRFTYGNQDLFATSQSKEFDPLGPLPPGWE
KRTDSNGRVYFVNHNTRITQWEDPRSQQQLNEKPLPEGWEMRFTVDGIPYFVDH
NRRTTTTYIDPRTGKSALDNGPQIA YVRDFKAKVQYFRFWCQQQLAMPQHIIKITVTR
KTLFEDSFQQIMSFSPQDLRRRLWVIFPGEEGLDYGGVAREWFFLLSHEVLNPMYC
5 LFEYAGKDNYCLQINPASYINPDHLKYFRFIGRFIAMALFHGKFIDTGFSLPFYKRIL
NKPVGKLDLESIDPEFYNSLIWVKENNIEECDLEMYFSVDKEILGEIKSHDLKPNGG
NILVTEENKEEYIRMVAEWRLSRGVEEQTQAFFEGFNEILPQQYLQYFDAKELEVL
LCGMQEIDLNDWQRHAIYRHYARTSKQIMWFWQFVKEIDNEKRMRLQLQFVTGTC
RLPVGGFADLMGSNGPQKFCIEKVGKENWLPRSHTCFNRDLPPYKSYEQLKEKL
10 LFAIEETEGFGQE

SEQ ID No:74 (Casein kinase III beta chain)

MSSSEEVSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILD
LEPDEELEDNPNQSDLIEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPR
15 VYCENQPMPLIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGA YFGTGFFH
MLFMVHPEYRPKRPANQFVPRLYGFKIHPMAYQLQLQAASNFKSPVKTR

SEQ ID No:75 (Cathepsin B)

MWQLWASLCCLLVLANARSRPSFHPVSEDLVNYVNKRNTTWQAGHNFYNVDMS
20 YLKRLCGTFLGGPKPPQRMFTEDLKLPA SFDAREQWPQCPTIKEIRDQGSCGSCW
AFGA VEAISDRICHTNAHVSVEVSAEDLLTCCGSMCGDGCNGGYPAEAWNFWTR
KGLVSGGLYESHVGC RPYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYK
QDKHYGYNSYSVSNSEKDIMA E IYKNGPVEGA FS VYSDFLLYKSGVYQHVTGEM
MGGHAIRILGWGVENGTPYWL VANSWNTDWGDNGFFKILRGQDHCGIESEVVAG
25 IPRTDQYWEKI

SEQ ID No:76 (Delta-6 fatt acid desaturase)

MGKGGNQGEGAAEREVSVP TFSWEEIQKHNLRTDRWLVIDRKVYNITKWSIQHP
GGQRVIGHYAGEDATDAFRA FHPDLEFVGKFLKPLLIGELAPEEPSQDHGKNSKIT
30 EDFRALRKTAEDMNLFKTNHVFFLLLLAHIIALESIAWFTVFYFGNGWIPTLITAFV
LATSQAQAGWLQHDYGHLSVYRKPKWNHLVHKFVIGHLKGASANWWNHRHFQ
HHAKPNIFHKDPDVNMLHV FVLGEWQPIEYGKKKLYLPYNHQHEYFFLIGPPLLI

PMYFQYQIIMTMIVHKNWVDLAWAVSYYIRFFITYIPFYGILGALLFLNFIRFLESH
WFWVWTQMNHIVMEIDQEAYRDWFSSQLTATCNVEQSFFNDWFSGHLNFQIEHH
LFPTMPRHNHLHKIAPLVKSLCAKHGIEYQEKPLLRAALLDIIRSLKKSGKLWLDAYL
HK

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SEQ ID No:77 (Nogo-A)

MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLER
KPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSP
VSSTVPAPSPLSAAA VSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPP
10 STPAAPKRRGSSSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSV
LLETAASLPSLSPLSAA SFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLL
IDRDLTEFSELEYSEMGSFSVSPKAESA VIVANPREEIIVKNKDEEEKLVSNILHN
QQELPTALTKLVKEDEVVSSEKAKDSFNEKRVA VEAPMREEYADFKPFERVWEV
KDSKEDSDMLAAGGKIESNLESKVDDKCFADSLEQTNHEKDSSESSNDDTSFPSTPE
15 GIKDRSGAYTTCAPFNPAATESIATNIFPLLGDPTSENKTDEKKIEEKKAAQIVTEKNT
STKTSNPFLVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNE
VTGTKIA YETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLN
SAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKE
PENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDHSSELVE
20 DSSPDSEPVDLFSDD SIPDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPP
EGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKKEKIPLQMEELSTAVYSNDDL FISC
AQIRETETFS DSSPIEIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSL
PCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVLPPDVSALATQAEIESIV
KPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGAS
25 LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAI
SEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFVLMWVFTYVGALFNGL
TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE

SEQ ID No:78 (PDGFRB)

30 MRLPGAMPALALKGELLLL SLLLLLEPQISQGLVVTPPGPELV LNVSSTFVLTCGS
APVVWERMSQEPPQEMAKAQDGTFSVLTLTNLTGLDTGEYFCTHNSRGLETDE
RKRLYIFVPDPTVGFLPND AEELFIFLTEITETPCRVTDPQLVVTLHEKKGDVALP

VPYDHQRGFSGIFEDRSYICKTTIGDREVDSDAYVYRLQVSSINVSVNAVQTVVR
QGENITLMCIVIGNEVVNFEWTYPRKESGRLVEPVTDFLLDMPYHIRSILHPSAELE
DSGTYTCNVTESVNDHQDEKAINITVVESGYVRLLEGEVGTLLQFAELHRSRTLQVV
FEAYPPPTVLWFKDNRTLGDSSAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYT
5 MRAFHEDAQVQLSFQLQINVPVRVLELSESHPSGEQTVRCRGRGMPQPNIIWSAC
RDLKRCPRELPPTLLGNSSEEEESQLETNVTYWEEEQEFVVSTLRLQHVDRLPSVR
CTLRNAVGQDTQEVIVVPHSLPFKVVVISAILALVVLTIISLILIMLWQKKPRYEIR
WKVIESVSSDGHEYTYVDPMQLPYDSTWELPRDQLVLGRTLGSAGFGQVVEATAH
GLSHSQATMKVAVKMLKSTARSSKQALMSELKIMSHLGPLNVNLLGACTKG
10 GPIYITEYCRYGDLVDYLHRNKHTFLQHHSKRRPPSAELYSNALPVGLPLPSHVS
LTGESDGGYMDMSKDESVDYVPMMLDMKGDVKYADIESSNYMAPYDNYVPSAPE
RTCRA TLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKL
VKICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEI
FTLGGTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFS
15 QLVLLLERLLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDLTSSVL
YTAVQPNEGDNDYIPLDPKPEVADEGPLGSPSLASSTLNEVNTSSTISCDSPLEP
QDEPEPEPQLELQVEPEPELEQLPDSGCPAPRAEAEDSFL

SEQ ID No:79 (ENSG00000144840)

20 MASLDRVKVLVLGDSGVGKSSLVHLLCQNQVLGNPSWTVGCSVDVRVHDYKEG
TPEEKTCYIELWDVGGSVGSASSVKSTRAVFYNSVNGIIFVHDLTNKKSSQNLRRW
SLEALNRDLVPTGVLVTNGDYDQEQFADNQIPLL VIGTKLDQIHETKRHEVLTTTA
FLAEDFNPEEINLDCTNPRYLAAGSSNAVKLSRFFDKVIEKRYFLREGNQIPGFPDR
KRFGAGTLKSLHYD

25

SEQ ID No:80 (PTK7)

MGAARGSPARPRRLPLSVLLPLLLGGTQTAIVFIKQPSSQDALQGRRALLRCEVE
APGPVHVYWLDDGAPVQDTERRFAQGSSLSFAAVDPLQDSGTFQCVARDDVTGE
EARSANASFNKWEIAGPVVLKHPASEAEIQPQTQVKLRCHIDGHPRPTYQWFRDG
30 TPLSDGQSNHTVSSKERNLTLRPAGPEHSGLYSCCAHSAFSQACSSQNFTLSIADES
FARVVLAPQDVVVARYYEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLRRAT
VFANGSLLLTVRPRNAGIYRCIGQGQGRGPPHLEATLHLAEIEDMPLFEPRVFTAGS

EERVTCCLPPKGLPEPSVWWEHAGVRLPTHGRVYQKGHELVLANIAESDAGVYTC
HAANLAGQRRQDVNITVATVPSWLKKPQDSQLEEGKPGYLDCLTQATPKPTVWV
YRNQMLISED SRFEVFKNGTLRINSVEVYDGTWYRCMSSTPAGSIEAQAVLQVLE
KLKFTPPPQPQCMGFDKEATVPCSATGREKPTIKWERADGSSSLPEWVTDNAGTL
5 HFARVTRDDAGNYTCIASNGPQGQIRAHVQLTVAVFITFKVEPERTTVYQGHTAL
LQCEAQGD PKPLIQWK GKDRILDPTKLGPRMHIFQNGSLVIHDVAPEDSGRYTCIA
GNSCNIKHTEAPLYVVDKPVPEESEGPSPPPYKMIQTIGLSVGAAVAYIIAVLGLM
FYCKKRCKAKRLQKQPEGEEPEMECLNGGPLQNGQPSAEIQEEVALTSLGSGPAA
TNKRHSTSDKMHFPRSSLQPITTLGKSEFGEVFLAKAQGLEEGVAETLVLVKSLQS
10 KDEQQQLDFRRELEMFGKLNHANVVRLLGLCREAEPHYMVLEYVDLEDLKQFLR
ISKSKDEKLSQPLSTKQKVALCTQVALGMEHLSNNRFVHKDLAARNCLVSAQR
QVKVSALGLSKDVYNSEYYHFRQAWVALRWMSPEAILEGDFSTKSDVWASGVL
MWEVFTHGEMPHGGQADDEV LADLQAGKARLPQPEGCP SKLYRLMQRCWALSP
KDRPSFSEIASALGDSTVDSKP

15

SEQ ID No:81 (FLJ13977)

MRRLTRRLVLPVFGVLWITVLLFFWVTKRKLEVPTGPEVQTPKPSDADWDDLWD
QFDERRY LNAKKWRVGDDPYKLYAFNQRESERISSNRAIPDTRHLSVLNRTPTHLI
REIILVDDFSNDPDDCKQLIKLPVKCLRNNERQGLVRSRIRGADIAQGTTLTFLDS
20 HCEVNRDWLQPLLHRVKEDYTRVVCVIDIINLDTFTYIESASELRGGFDWSLHFQ
WEQLSPEQKARRLDPTPIRTPIIAGGLFVIDKAWFDYLGKYDMDMDIWGGENFEI
SFRVWMC GGSLEIVPCSRVGHVFRKKHPYVFPDGNANTYIKNTKRTAEVWMDEY
KRYYYAARPFALERPFGNVESRLDLRKNLRCQSFKWYLENTYPELSIPKESSIQKGN
IRQRQKCLESQANGTTGSSGQRPAGGTSEIWVQKPRVRNRRHAAPQGFDPGAKPS
25 QHWRRPEHPAAE

SEQ ID No:82 (FLJ20481)

MFFSMGFIVAVKGKIASPLEAPVFVAAPHSTFFDGIACVVAGLPSMVSRNENAQVP
LIGRLLRAVQPVLSRVDPDSRKNTINEIHKRTTSGGEWPQILVFPEGTCTNRSCLIT
30 FKPGAFIPGVPVQPVLLRYPNKLDVTWTWQGYTFIQLCMLTFCQLFTKVEVEFM
PVQVPNDEEKNDPVL FANKVRNLMAEALGIPVTDHTYEDCRLMISAGQLTLPMEA
GLVEFTKISRKLKLDWDGVRKHLDEYASIASSSKGGRIIEEFAKYLKLPVSDVLR

QLFALFDRNHDGSIDFREYVIGLAVLCNPSNTEEEIQVAFKLFDVDEDGYTTEEEFST
ILQASLGVPDLDVSGLFKEIAQGDSISYEFEKSFALKHPEYAKIFTTYLDLQTCNVFS
LPKEVQTTTPSTASNKVSPEKHEESTSDKKDD

5 SEQ ID No:83 (SERPINA1)

MPSSVSWGILLLAGLCCLVPVSLAEDPQGDAQAQKTDTSHTDQDHPTFNKITPNLA
EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTPEI
AQIHEGFQELLRTLNPDSQLQLTTGNGLFLSEGLKLVDFLEDVKKLYHSEAFV
NFGDTEEAQKQINDYVEKGTQGGKIVDLVKELDRDTVFALVNYIFFKGKWERPFV
10 KDTTEEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSSWVLLMKYLGNAITFFL
PDEGKLQHLENELTHDITKFLNEDRRSASLHLPKLSITGTDLKSVLGQLGITKV
FSNGADLSGVTEEAPLKLSKAVHKA VLTIDEKGTEAAGAMFLEAIPMSIPPEVKFN
KPFVFLMIEQNTKSPLFMGKVVNPTQK

15 SEQ ID No:84 (FLJ22390)

MRPRRPHQIADLFRPKDQIAYS DTS PFLILSEASLADLNSRLEKKVKATNFRPNIVIS
GCDVYAEDSWDELLIGDVELKRVMACSRCILTTVDPDTGVMSRKEPLETLKSYRQ
CDPSEKLYGKSPLFGQYFVLENPGTIKVGDPVYLLGQ

20 SEQ ID No:85 (SIM TO Y71H10A. 2.P.)

MVSIPEYYEGKNVLLTGATGFLGKVLLEKLLRSCPKVNSVYVLRQKAGQTPQER
VEEVLSGKLFDRRLDENPDFREKIIAINSELTQPKLALSEEDKEVIDSTNIIFHCAAT
VRFNENLRDAVQLNVIATRQLILLAQQMKNLEVMHVSTAYAYCNRKHIDEVY
PPPVDPKKLIDSLEWMDDGLVNDITPKLIGDRPNTYITKALAEYVVQQEGAKLN
25 VAIVRPSIVGASWKEPFPGWIDNFGPSGLFIAAGKGILRTIRASNNALADLVPVDV
VVNMSLAAA WYSGVNRPRNIMVYNCTTGSTNPFHWGEVEYHVISTFKRNPLEQA
FRPNVNLTSNHLLYHYWIAVSHKAPAFLYDIYLRMTGRSPRCPSFKFNSNSLSHH
YRKGVSHRVSALLDCTHVDRSETATFNIDVRQLHWA EYIENYCLGTTKKYVLNEE
MSGPLAARKHLNKTLSLFTALCHGKLT FVDDTFGFPCLLASGGPLLSVSLHFS
30 YVYSQIHLAFILRDLGSHSAPSLASLAGPRELTVGSLLDREWRQIKTDDFELGKSAG
EVDLEGADIEGCLLATSPA VRQQALLQRGVQWYISIPTTQETVAMEMQI

SEQ ID No:86 (Hypothetical protein tyrosine phosphatase ensg00000149185)

MAATALLEAGLARVLFYPTLLYTLFRGKVPGRAHRDWHRIDPTVLLGALPLRSL
TRQLVQDENVRGVITMNEEYETRFLCNSSQEWKRLGVEQLRLSTVDMTGIPTLDN
LQKGVQFALKYQSLGQCVYVHCKAGRSRSATMVAAYLIQVHKWSPEEAVRAIAK
5 IRSYHIRPGQLDVLKEFHKQITARATKDGTFFVISK

SEQ ID No:87 (ICAM-2)

MSSFGYRTLTVLFTLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPE
VGGLTSLNKKILLDEQAQWKHYLVSNISHDTVLCCHFTCSGKQESMNSNVSVYQP
10 PRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAP
QEATATFNSTADREDGHRNFSCLAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQ
MVIIVTVVSVLLSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP

SEQ ID No:88 (KIAA1181)

15 ASGEWRVSGGRPAGAGRPEEALAAGSDPRGAAARLACSAPTPGGGTMPDFRRF
DIYRKVPKDLTQPTYTGAIIISCCCLFILFLFLSELTGFITTEVVNELYVDDDPKDSGG
KIDVSLNISLPLNLHCELVGLDIQDEMGRHEVGHIDNSMKIPLNNGAGCRFEGQFSIN
KVPGNFHVSTHSATAQPQNPDMTHTVHKLSFGDTLQVQNIHGAFNALGGADRLTS
NPLASHDYILKIVPTVYEDKSGKQRYSYQYTVANKEYVAYSHTGRIIPAIWFRYDL
20 SPITVKYTERRQPLYRFITTICAIIGGTFTVAGILDSCIFTASEAWKKIQLGKMH

SEQ ID No:89 (KIAA1533)

NSKKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQREILLQGRLY
LSEWICFYFYSNIFRWETTISIQKEVTCLKKEKTAKLIPNAIQICTESEKHFFTSFGAR
25 DRCFLIFRLWQNALLEKTLSPRELWHLVHQCYGSELGLTSEDEDYVSPLQLNGL
GTPKEVGDVIALSDITSSGAADRSQEPSVGSRRGHVTPNLSRASSDADHGAEEDK
EEQVDSQPDASSSQTVTPVAEPPSTEPTQPDGPTTLGPLDLLPSEELLTDTSNSSSST
GEEADLAALLPDLSGRLLINSVFHVGAERLQQMLFSDSPFLQGFLQCKFTDVTLS
PWGDSKCHQRRVLTYTIPISNPLGPKSASVVETQTLFRRGPQAGGCVVDSSEVLQ
30 GIPYQDYFYTAHRYCILGLARNKARLRVSSEIRYRKQPWSLVKSLIEKNSWSGIED
YFHHLERELAKAEKLSLEEGGKDARGLLSGLRRRKRPPLSWRAHGDGPQHPDPDPC
ARAGIHTSGSLSSRFSEPSVDQGPAGIPSAVLISIVSLIILIALNVLLFYRLWSLERT

AHTFESWHSALAKGKFPQTATEWAEILALQKQFHSVEVHKWRQILRASVELLDE
MKFSLEKLHQGITVSDPPFDTQPRPDDSFS

SEQ ID No:90 (kinectin 1 (kinesin receptor))

5 MEFYESA YFIVLIPSIVTVIFLFFWLFMKETLYDEV LAKQKREQKLIPTKTDKKKAE
KKKNKKKEIQNGNLHESDSES VPRDFKLSDALA VEDDQVAPVPLNVVETSSSVRE
RKKKEKKQKPVL EEQVIKESDASKIPGKKVEPVPTKQTPPSEAAASKKKPGQK
KSKNGSDDQDKK VETLMVPSKRQEALPLHQETKQESGSGKKASSKKQKTENVFV
DEPLIHATTYIPLMDNADSSPVVDKREVIDLLKPDQVEGIQKSGTKKLKTETDKEN
10 AEVKFKDFLLSLKTMMFSEDEALCVVDLLKEKSGVIQDALKKSSKGELTTLIHQLO
EKDKLLAAVKEDAAATKDRCKQLTQEMMTEKERSNVVMTRMKDRIGTLEKEHN
VFQNKIHVS YQETQQMQMKFQQVREQMEAEIAHLKQENGILRDAVSNTTNQLES
KQSAELNKL RQDYARLVNELTEKTGKLQQEEVQKKNAEQAAATQLKVQLQEAERR
WEEVQSYIRKRTAEHEAAQQDLQSKFVAKENEVQSLHSKLTDTLVSKQQLEQRL
15 MQLMESEQKRVNKEESLQMQVQDILEQNEALKAQIQQFHSQIAAQT SASVLA EEL
HKVIAEKDKQIKQTEDSLASERDRLTSKEELKDIQNMNFLKAEVQKLQALANE
QAAAAHELEKMQQSVYVKDDKIRLLEEQLQHEISNKMEEFKILNDQNKALKSEVQ
KLQTLVSEQPNKDVVEQMEKCIQEKDEKLKTVEELLE TGLIQVATKEEELNAIRTE
NSSLTKEVQDLKAKQNDQVSFASLVEELKKVIHEKDGKIKSVEELLEAE LLKVAN
20 KEKTVQDLKQEIKALKEEIGNVQLEKAQQLSITSKVQELQNLLKGKEEQMNTMKA
VLEEKEKDLANTGKWLQDLQEENESLKAHVQEVAQHNLKEASSASQFEELEIVLK
EKGNELKRLEAMLKERESDLSSKTQLLQDVQDENKLFKSQIEQLKQQNYQQASSF
PPHEELLKVISEREKEISGLWNE LDSLKDAVEHQ RKKNNDLREKNWEAMEALAST
EKMLQDKVNKTSKERQQQVEAVELEAKEVLKCLF PKVSVPSNLSYGEWLHGFEK
25 KAKECMAGTSGSEEVKVLEHKLKEADEMH TLLQLECEKYKSVLAETEGILQKLQ
RSVEQEENKWKVKVDESHKTIKMQSSFTSSEQELERLRSENKD IENLRREHLE
MELEKAEMERSTYVTEVRELKDLLTELQKKLDDSYSEAVRQNEELNLLKAQLNET
LTKLRTEQNERQKVAGDLHKAQQSLELIQSKIVKAAGD TTVIENS DVSPETESSEK
ETMSVSLNQTVTQLQQLLQAVNQQLTKEKEHYQVLE

30

SEQ ID No:91 (Mesenchymal stem cell protein DSCD75)

MLGLLVALLALGLAVFALLDVWYLVRLPCAVLRARLLQPRVRDLLAEQRFPGRV
LPSDLDLLLHMNNARYLREADFARVAHLTRCGVLGALRELRAHTVLAASCARHR
RSLRLLEPFVVRTRLLGWDDRAFYLEARFVSLRDGFVCALLRFRQHLLGTSPERVV
QHLCQRRVEPPELPADLQHWISYNEASSQLRMESGLSDVTKDQ

5

SEQ ID No:92 (Neurotrypsin)

MTLARFVLALMLGALPEVVGFDVSLNDSLHSHSRHSPPAGPHYPPYLPTQQRPT
TRPPPPLPRFPRPPRALPAQRPHALQAGHTPRPHPWGCPAGEPWVSVTDFGAPCLR
WAEVPPFLERSPPASWAQLRGQRHNFCSRSPDGAGRPWCIFYGDARGKVDWGYCD
10 CRHGSVRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGI
AKQTPFSGGLIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCFSFH
GPTFPIIRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADADEVICRQLGLSGIAK
AWHQAYFGEGSGPVMLEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSCTPL
TDGVIRLAGGKGSHGRLEVYYRGQWGTVCDDGWTELNTYVVCRLGFKYKGKQ
15 ASANHFEESTGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGGE
GHRLSLGFPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYK
GPARARTMAYFGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC
DYFGKKASGNSNKESSLSSVCGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSH
GDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEEFEEEEIGV
20 QQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQKTASNC
YITGWGDTGRAYSRTLQQAAPLLPKRFCEERYKGRFTGRMLCAGNLHEHKRVDS
CQGDSSGGLMCERPGEWVVYGVTSWGYCGVKDSPGVYTKVSAFVPWIKSVT
KL

25 SEQ ID No:93 (PP1, regulatory subunit 15B)

MEPGTGGSRKRLGPRAGFRFWPPFFPRRSQAGSSKFPTPLGPENSGNPTLLSSAQPE
TRVSYWTKLLSLLAPLPGLLQKVLWSQLFGGMFPTRWLDFAGVYSALRALKGR
EKPAAPTAQKSSSLQLDSSDPSVTSPLDWLEEGIHQYSPDLKLELKAKGSALD
PAAQAFLEQQLWGVLLPSSLQSRLYSNRELGSSPSGPLNIQRIDDFS VVS YLLNP
30 SYLDCFPRLVSYQNSDGNSEVVGFTLTPESSCLREDHCHPQPLSAELIPASWQG
CPPLSTEGLPEIHHLRMKRLEFLQQAASKGQDLPTPDQDNGYHSLEEEHSLLRMDPK
HCRDNPTQFVPAAGDIPGNTQESTEEKIELLTTEVPLALEEESPSEGCPSSSEIPMEKE

PGEGRISVVDYSYLEGDLPIARPACSNKLIDYILGGASSDLETSSDPEGEDWDEEA
EDDGFSDSSSLSDSDLEQDPEGLHLWNSFCSVDPYNPQNFTATIQTAAARIVPEEPPSD
SEKDLGKSDLENSSQSGSLPETPEHSSGEEDDWESSADEAESLKLWNSFCNSDDP
YNPLNFKAPFQTSGENEKGCRDSKTPSESVASECHTLLSCKVQLLGSQSESECPDS
5 VQRDVLSSGGRHHTHVKRKKVTFLEEVTEYYISGDEDRKGPWEEFARDGCRFQKRIQ
ETEDAIGYCLTFEHRERMFNRLQGTCFKGLNVLKQC

SEQ ID No:94 (Protein amplified in osteosarcoma (OS-9))

MAAETLLSSLLGLLLLGLLLPA SLTG GVS LNLEELSEMRYGIEILPLPVMGGQSQS
10 SDVVIVSSKYKQRYECRLPAGAIHFQREREEETPAYQGPGIPELLSPMRDAPCLLKT
KDWWTYEFCYGRHIQQYHMEDSEIKGEVLYLGYYSQAFDWDEETAKASKQHRL
KRYHSQTYGNGSKCDLNGRPREAEVRFLCDEGAGISGDYIDRVDEPLSCSYVLTR
TPRLCPHPLL RPPPSAAPQAILCHPSLQPEEYMA YVQRQADSKQYGDKIEELQDLG
PQVWSETKSGVAPQKMAGASPTKDDSKDSDFWKMLNEPEDQAPGGEEVPAEEQ
15 DPSPEAADSASGAPNDFQNNVQVKVIRSPADLIRFIEELKGGTKKGKPNIGQEOPV
DDAAEVPQREPEKERGDPERQREMEEEDEDEDEDEDERQLLGEFEKELEGILL
PSDRDRLRSEVKAGMERELENIIQETEKELDPDGLKKESERDRAMLALTSTLNKLI
KRLEEKQSPELVKKHKKKRVVPKKPPSPQPTTEEDPEHRVRVRVTKLRLGGPNQD
LTVLEMKREN PQLKQIEGLVKELLEREGLTAAGKIEIKIVRPWAEGTEEGARWLTD
20 EDTRNLKEIFFNILVPGAEEAQKERQRQKELESNYRRVWGSPGGEGTGDLDEFDF

SEQ ID No:95 (Protein similar to stromal cell-derived factor 2)

MAVVPLLLLGLWSAVGASSLGVVTCGSVVKLLNTRHNVRLHSHDVRYGSGSGQ
QSVTGVTSDDSNSYWRIRGKSATVCERGTPIKCGQPIRLTHVNTGRNLHSHHFTS
25 PLSGNQEVS AFGEEGEGDY LDDWTVLCNGPYWVRDGEVRFKHSSTEVL SVTGE
QYGRPISGQKEVHGMAQPSQNNYWKAMEGIFMKPSELLKAEAHHAEL

SEQ ID No:96 (Protocadherin beta 8)

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLA KDLGLE
30 QREFSRRGVRVVS RGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLR FQVLL
ESPFEFFQAE LQVIDINDHSPVFLDKQMLVKVSESSPPGTAFPLKNAEDLDIGQNNI
ENYIISPNSYFRVLTRKRS DGRKYPELVLDNALDREEEAELRLTLTALDGGSPPRS G

TAQVYIEVVDVNDNAPEFQQPFYRVQISEDSPISFLVVKVSATDVDVTGVNGEISYSL
FQASDEISKTFKVDFLTGEIRLKKQLDFEKFQSYEVNIEARDAGGFSGKCTVLIQVI
DVNDHAPEVTMSAFTSPIPENAPETVVALFSVSDLDSENGKISCSIQEDLPFLKSS
VGNFYTLLTETPLDRESRAEYNVTITVTDLGTPRLTTHLNMTVLVSDVNDNAPAF
5 QTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDPHPLASLVSINTD
NGHLFALRSLDYEALQAFEFVVGASDRGSPALSSEALVRVLVLDANDNSPFVLYPL
QNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVW
AHNGEVRTARLLSERDAAKQRLVVLVKDNGEPPCSATATLHLLLVDFGSQPYLPL
PEAAPAQGGADSLTVYLVALASVSSLFLFSVLLFVAVLLCRRSRAASVGRCSVPE
10 GPFPGHLVDVRGTGSLSQNYQYEVCLAGGSGTNEFQFLKPVLPNIQGHSGPPEME
QNSNFRNGFGFSLQLK

SEQ ID No:97 (REP8 protein)

MASRGVVGIFFLSAVPLVCLLELRGIPDIGIKDFLLCGRILLALLTLISVTTSWL
15 NSFKSPQVYLKEEEEKNEKRQKLVRKKQQEAQGEKASRYIENVLKPHQEMKLK
LEERFYQMTGEAWKLSSGHKLGGDEGTSQTSFETSNREAAKSQNLKPLTEFFSPA
EQPTCKEIPDLPEEPSQTAEVVTVALRCPSGNVLRRLFLKSYSSQVLFDMTRIG
YHISLYSLSTSFPRLPLAVEGGQSLEDIGITVDTVLLEEKEQTN

20 SEQ ID No:98 (RING finger protein 5)

MAAAEEEDGGPEGPNRERGGAGATFECNICLETAREAVVSVCGHLYCWPC LHQW
LETRPERQECVPCKAGISREKVPLYGRGSQKPQDPRLKTPPRPQGQRPAPESRGG
FQPFGDTGGFHFSGVGAFFPGFFTTVFNAHEPFRRGTGVDLGQGHPASSWQDSL
LFLAIFFFWLLSI

25

SEQ ID No:99 (Retinal short-chain dehydrogenase/reductase retSDR2)

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTA YEFAKL
KSKLVLDINKHGLEETAACKGLGAKVHTFVVDCSNREDIYSSAKKVKA EIGD
VSILVNNAGVVYTSDLFATQDPQIEKTFEVNVL AHFWTTKAFLPAMTKNNHGHIV
30 TVASAAGHVSVPFLLAYCSSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNT
GFIKNPSTSLGPTLEPEEVNRLMHGILTEQKMIFPSSIAFLTTLERILPERFLAVLK
RKISVKFDAVIGYKMAQ

SEQ ID No:100 (Stromal cell-derived factor 2-like 1)

MWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRL
HSHDIKYGSGSGQSVTGVEASDDANSYWRIRGGSEGGCPCGSPVRCGQAVRLTH
5 VLTGKNLHTHHFPSPLSNNQEVSAFGEDGEGDDLDLWTVRCSGQHWEREAAVRL
QHVGTSVFLSVTGEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAG
HDEL

SEQ ID No:101 (Thioredoxin domain-containing protein)

10 GRWASGEMAPSGSLAVPLAVLVLLWLGAPWTHGRRSNVRVITDENWRELLEGD
WMIEFYAPWCPACQNLQPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFITALPT
IYHCKDGEFRRYQGPRTKKDFINFISDKWKSEIPVSSWFGPGSVLMSSMSALFQLS
MWIRTCHNYFIEDLGLPVWGSYTVFALATLFSGLLLGLCMIFVADCLCPSKRRRPQ
PYPYPSKKLLSESAQPLKKVEEEQEADEEDVSEEEAESKEGTNKDFPQNAIRQRSL
15 GPSLATDKS

SEQ ID No:102 (Voltage-dependent anion channel 1)

AVPPTYADLGKSARDVFTKGYGFGLIKLDLKTSENGLEFTSSGSANTETTKVTGS
LETKYRWTEYGLTFTEKWNTDNTLGTEITVEDQLARGCLKLTFDSSFPNTGKKNA
20 KIKTGYKREHINLGCDMDFDIAGPSIRGALVLGYEGWLAGYQMNFETAKSRVTQS
NFAVGKYKTDEFQLHTNVNDGTEFGGSIYQKVNKKLETA VNLAWTAGNSNTRFGI
AAKYQIDPDACFSAKVNNSSLIGLGYTQTLKPGIKLTLALLDGKNVNAGGHKLG
LGLEFQA

25 SEQID No:103 (ATP-binding cassette, sub-family A member 3)

MAVLRQLALLLWKNYTLQKRKVLVTVLELFLPLLFPGLIWLRLKIQSENVPNATI
YPGQSIQELPLFFTFPPPGDTWELAYIPSHSDAAKTVTETVRRALVINMRVRGFPSE
KDFEDYIRYDNCSSSVLAAVVFEHPPFNHSKEPLPLAVKYHLRFSYTRRNYMWTQT
GSFFLKETEGWHTTSLFPLFPNPGPRELTSPDGGEPGYIREGFLAVQHAVDRAIME
30 YHADAATRQLFQRLTVTIKRFPYPPFIADPFLVAIQYQLPLLLLLSFTYTALTIAARAV
VQEKERRLKEYMRMMGLSSWLHWSAWFLFFLFLIAASFMTLLFCVKVKNVA
VLSRSDPSLVLAFLLCFAISTISFSFMVSTFFSKANMAAAFGGFLYFFTYIPYFFVAP

RYNWMTLSQKLCSCLLSNVAMAMGAQLIGKFEAKGMGIQWRDLLSPVNVDDDF
CFGQVLGMLLLDSVLYGLVTWYMEAVFPGQFGVPQPWYFFIMPSYWCGKPRAV
AGKEEEDSDPEKALRNEYFEAEPEDLVAGIKIKHLSKVFRVGNKDRAAVRDLNLN
LYEGQITVLLGHNGAGKTTTSLMTGLFPPTSGRAYISGYEISQDMVQIRKSLGLCP
5 QHDILFDNLTVAEHLFYFAQLKGLSRQKCPEEVKQMLHIIGLEDKWNRSRSLSG
GMRRKLSIGIALIAGSKVLILDEPTSGMDAISRAIWDLLQRQKSDRTIVLTTHFMD
EADLLGDRIAIMAKGELQCCGSSLFLKQKYGAGYHMTLVKEPHCNPEDISQLVHH
HVPNATLESSAGAELSFIIPRESTHRFEGLFAKLEKKQKELGASFGASITTMEEVFL
RVGKLVDSMDIQAIQLPALQYQHERRASDWA VDSNLCGAMDPDGDIGALIEEER
10 TAVKLNTGLALHCQQFWAMFLKKAAYSWREWKMVAAQVLVPLTCVTLALLAIN
YSSELFDDPMLRLTLGEYGRTVVPFSVPGTSQLGQQLSEHLKDALQAEGQEPREV
LGDLEEFLIFRASVEGGGFNERCLVAASFRDVGERTVVNALFNNQAYHSPATALA
VVDNLLFKLLCGPHASIVVSNFPQPRSAQAQKQDNFNEGRKGFIDIALNLLFAMAFL
ASTFSILAVSERAVQAKHVQFVSGVHVASFWSALLWDLISFLIPSLLLL VVFKAFD
15 VRAFTRDGHMADTLLLLLLYGWAIPLMYLMNFFFLGAATAYTRLTIFNLSGIATF
LMVTIMRIPAVKLEELSKTLDHVFVLVLPNHCLGMAVSSFYENYETRRYCTSSEVA
AHYCKKYNIQYQENFYAWSAPGVGRFVASMAASGCAYLILLFLIETNLLQRLRGIL
CALRRRRTLTEL YTRMPVLPEDQDVADERTRILAPSPDSSLHTPLIKELSKVYEQR
VPLLAVDRLSLAVQKGECFGLLGFGAGKTTTFKMLTGEESLTSGDAFVGGHRISS
20 DVGKVRQRIGYCPQFDALLDHMTGREMLVMYARLRGIPERHIGACVENTLRGLLL
EPHANKLVRTYSGGNKRKLSTGIALIGEPAVIFLDEPSTGMDPVARRLLWDTVARA
RESGKAIIITSHSMEECEALCTRLAIMVQGQFKCLGSPQHLKSKFGSGYSLRAKVQS
EGQQEALIEEFKAFVDLTFPGSVLEDEHQGMVHYHLPGRDLSWAKVFGILEKAKE
KYGVD DYSVSQISLEQVFLSFAHLQPPTAEGR

25

SEQID No:104 (CAMK4)

MLKVTVPSCSASSCSSVTASAAPGTASLVPDYWIDGSNRDALSDFFEVESELGRGA
TSIVYRCKQKGTQKPYALKVLKKTVDKKIVRTEIGVLLRLSHPNIIKLKEIFETPTEI
SLVLELVTGGELFDRIVEKGYYSERDAADAVKQILEAVAYLHENGIVHRDLKPEN
30 LLYATPAPDAPLKIADFGLSKIVEHQVLMKTVCGTPGYCAPEILRGCAYGPEVDM
WSVGITYILLCGFEPFYDERGDQFMFRILNCEYYFISPPWWDEVSLNAKDLVRKLI
VLDPKKRLTTFQALQHPWVTGKAANFVHMDTAQKKLQEFNARRKLKAAVKAVV

ASSRLGSASSSHGSIQESHKASRDPSPIQDGNEDMKAIPERGEKIQGDGAQAAVKGA
QAEMLMKVQALEKVKGADINAEEAPKMVPKAVEDGIKVADLELEEGLAEEKLKTV
EEAAAPREGQGSSAVGFEVPQQDVILPEY

5 SEQ ID No:105 (KIAA0363)

EPCALTPGPSHLALTFLPSKPGARPQPEGASWDAGPGGAPSAWADPGEGGPSML
LPEGLSSQALSTEAPLPATLEPRIVMGEETCQALLSPRAARTALRDQEGGHASPDPP
PELCSQGDLSVPSPPDPDSFFTPPSTPTKTTYALLPACGPHGDARDSEAELRDELL
DSPPASPSGSYITADGDSWASSPSCSLSLAPAEGLDFPSGWGLSPQGSVMDEREL
10 HPAGTPEPPSSSESSLADSSSSWGQEGHFFDLDFLANDPMPAALLPFQGSILFQVE
AVEVTPLSPEEEEEEA VADPDPGDLAGEGEEDSTSASFQSLSDLSITEGMDEAFA
FRDDTSAASSSDSDSASYAEADDERLYSGEPHAQATLLQDSVQKTEESGGGAKGL
QAQDGTVSWAVEAAPQTSDRGAYLSQRQELISEVTEEGLALGQESTATVTPHTLQ
VAPGLQVEVATRVTTPQAGEEETDSTAGQESAAMAMPQPSQEGISEILGQESVTAE
15 KLPTPQEETSLTLCPDSPQNLKEEGGLDLPSGRKPVAAATIVPRQAKEDLTL PQDSA
MTPPLPLQD TDLSSAPKPVAAATIVSQQAEGLTLPQDSVMTPPLPLQDTELSSAPK
PVAAATLVSQQAEGLTLPQDSAMTPPLPLQD TDLSSAPKPVAAATLVSQQAEGL
LTLPQDSAMTPPLPLQD TDLSSAPKPVAAATLVSQQAEGLTLPQDSAMTPPLPLQ
D TDLSSAPKPVAAATIVSQQAEGLTLPQDSAMTPPLPLQD TDLSSAPKPVAAATI
20 VSQQAEGLTLPQDSAMTPPLPLQD TDLSSAPKPVAAATPVVSQQAEGLTLPQDSA
MTPPLPLQD TDLSSAPKPVAAATPVVSQQAEGLTLPQDSAMTAPLPLQDTGPTSGP
EPLAVATPQTLQAEAGCAPGTEPVATMAQQEVGEALGPRPAPEEKNAALPTVPEP
AALDQVQQDDPQPAEAGTPWAAQEDADSTLGMEALSLPEPASGAGEEIAEALSR
PGREACLEARAHTGDGAKPDSPQKETLEVENQQEGGLKLLAQEHGPRSA LGGAR
25 EVPDAPPAACPEVSQARLLSPAREERGLSGKSTPEPTLPSAVATEASLDSCPESSVG
AVSSLDRGCPDAPAPTSAPTSQQPEPVLGLGSVEQPHEVPSVLGTPLLQPPENLAK
GQPSTPVDRPLGPDPSAPGTLAGAALPPLEPPAPCLCQDPQEDSVEDEEPPGSLGLP
PPQAGVQPAAAAVSGTTQPLGTGPRVSLSPHSPLSPKVASMDAKDLALQILPPCQ
VPPPSGPQSPAGPQGLSAPEQQEDEDSEEDSPRALGSGQHSDSHGESSAELDEQDI
30 LAPQTVQCPAQAPAGGSEETIAKAKQSRSEKKARKAMSKLGLRQIQGVTRITIQKS
KNILFVIAKPDVFKSPASDTYVVFGEAKIEDLSQQVHKAAAEKFKVPSEPSALVPES

APRPRVRLECKEEEEEEEEVDEAGLELRDIELVMAQANVSRAKAVRALRDNHSD
IVNAIMELTM

SEQID No:106 (DCTN1)

5 MMRQAPTARKTTTTRPKPTRPASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTP
LAAPIIPTPVLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKAKLKE
LEKHKIQLEQVQEWKSKMQEQQADLQRRLEKEARKEAKEALEAKER YMEEMADT
ADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEKGS DGAAS
SYQLKQLEEQNARLKDALVRMRDLSSEKQEHVKLQKLMEKKNQELEVVRRQRE
10 RLQEELSQAESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDLE
AMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAAQETVADYQQTIK
KYRQLTAHLQDVNREL TNQQEASVERQQQPPPETFDKIKFAETKAHAKAIEMEL
RQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCVLVLLMPRLICKAELIRKQAAQ
EKFELSENC SERPGLRGAAQEQLSFAAGLVYSLSLQATLHRYEHALSQCSVDVY
15 KKVGSLYPEMSAHERSLDFLIELLHKDQLDET VNVEPLTKAIKYYQHLYSIHLAEQ
PEDCTMQLADHIKFTQSALDCMSVEVGRLRAFLQGGQEATDIALLLRDLETSCSDI
RQFCKKIRRRMPGTDAPGIPAALAFGPQVSDTLDCRKH LTWVVAVLQEVA AAA
AQLIAPLAENEGLLVA ALEELAFKASEQIYGTPSSSPYECLRQSCNLISTMKNLAT
AMQEGEYDAERPPSKPPPVELRAAALRAEITDAEGLGLKLEDRET VIKELKKS LKI
20 KGEELSEANVRLS LLEKKLDSA AKDADERIEKVQTRLEETQALLRKKEKEFEETM
DALQADIDQLEAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQRGAI
PGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSILKGAQMKASLASLPPL
HVAKLSHEGPGSEL PAGALYRKTSQLLETNLQLSTHTHVVDITRTSPA AKSPSAQL
MEQVAQLKSLSDTVEKLKDEV LKETVSQRPGATVPTDFATFPSSAFLRAKEEQQD
25 DTVYMGKVTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS

SEQ ID No:107 (KIAA1250)

LQLSVKMSVLISQSVINYVEENIPALKALLEKCKDVDERNECGQTPLMIAAEQGN
LEIVKELIKNGANCNLEDLDNWTALISASKEGHVHIVEELLKCGVNLEHRDMGGW
30 TALMWACYKGR TDVV ELLLSHG ANPSVTGLYSVYPIIWAAGRGHADIVHLL LQN
GAKVNCSDKYGTTPLVWAARKGHLECVKHLLAMGADVDQEGANSMTALIVAV
KGGYTQSVKEILKRNP NVNLTDKDGNTALMIASKEGHTEIVQDLLDAGTYVNPID

RSGDTVLI GAVRGGHVEIVRALLQKYADIDIRGQDNKTALYWAVEKGNATMVRD
ILQCNPDTEICTKDGETPLIKATKMRNIEVVELL LDKGAKVSAVDKKGDTPLHIAIR
GRSRKLAELL LRNP KDGRLLYRPNKAGETPYNIDCSHQKSILTQIFGARHLSPTETD
GDMLGYDLYSSALADILSEPTMQPPICVGLYAQWGS GKSFL LKKLEDEMKT FAGQ
5 QIEPLFQFSWLIVFL TLLLCGGLGLLFAFTVHPNLGIAVSL SFLALLYIEFFIVYFGGR
REGESWNWAWVLSTRLARHIGYLELL LKLMFVNPPELPEQTTKALPVRFLFTDYN
RLSSVGGETSLAEMIATLSDACEREFGLATRLFRVFKTEDTQ GKKKWKKTCCCLPS
FVIFLFIIGCIISGITLLAIFRVDPKHLTVNAV LISIASVVGLAFVLNCR TWQVLD SL
LNSQRKRLHNAASKLHKLKSEGFMKVLKCEVELMARMAKTIDSFTQNQTRLV VII
10 DGLDACEQDKVLQMLDTVRVLFSKGPFIAIFASDPHIIKAINQNLNSVLRDSNING
HDYMRNIVHLPVFLNSRGLSNARKFLVTSATNGDVPCSDTTGIQEDADRRVSQNS
LGEMTKLGSKTALNRRDTYRRRQMQR TITRQMSFDLTKLLVTE DWFSDISPQTMR
RLNIVSVTGRLLRANQISFNWDR LASWINLTEQWPYRTSWL LYLEETEGIPDQM
TLKTIYERISKNIPTTKDVEPLLEIDGDIRNFEVFLSSRTPVLVARDVKVFLPCTVNL
15 DPKLREIIADVRAAREQISIGGLAYPPLPLHEGPPRAPSGYSQPPSVCSSTS FN GPFA
GGVVSPQPHSSYSGMTGPQHFPYNRPFAPYL YTPRYYPGGSQHLSRPSVKTS L
PRDQNNGLEVIKEDAAEGLSSPTDSSRGS GPAGPVLLNSLNVDAVCEK LKQIEG
LDQSM LPQYCTTIKKANINGR VLAQCNIDELKKEMNMNFGDWHLFRSTVLEM RN
AESHVVPEDPRFLSESSSGPAPHGEPARRASHNELPHTELSSQTPYTLNFSFEELNTL
20 GLDEGAPRHSNLSWQSQTRRTPSLSSLNSQDSSIEISKLT DKVQAEYRDAYREYIAQ
MSQLEGGPGSTTISGRSSPHSTYYMGQSSSGGSIHSNLEQEKGKDSEPKPDDGRKSF
LMKRGDVIDYSSSGVSTNDASPLDPITEEDEKSDQSGSKLLPGKKSSERSSLFQTDL
KLKGSGLRYQKLPSDEDESGTEESDNTPLLKDDKDRKAEGKVERVPKSPEHSAEPI
RTFIKAKEYLSDALLDKKDSSDSGVRSSSESPNHS LHNEVADDSQLEKANLIELED
25 DSHSGKRGIPHSLSGLQDPHARM SICS EDDKSPSECSLIASSPEENWPACQKAYNLN
RTPSTVTLNNSAPANRANQNFD EMEGIRETSQVILRPSSSPNPTTIQENENLKSMT H
KRSQRSSYTRL SKDPPELHAAASSESTGFGEERESIL

SEQID No:108 (FACL3)

30 MNNHVSSKPSTMKLKHTINPILLYFIHFLISLYTILTYIPFYFFSES RQEKS NRIKAKP
VNSKPD SAYRSVNSLDGLASVLYPGCDTLDKVFTYAKNKFKNKRL LGTREVLNEE
DEVQPNGKIFKKVILGQYNWLSYEDVFVRAFNFNGNLQMLGQKPKTNIAIFCETR

AEWMIAAQACFMYNFQLVTLYATLGGPAIVHALNETEVTNIITSKELLQTKLKDIV
SLVPRLRHITVDGKPPTWSDFPKGIIVHTMAAVEALGAKASMENQPHSKPLPSDIA
VIMYTSGSTGLPKGVMISHSNIIAGITGMAERIPELGEEDVYIGYLPLAHVLELSAEL
VCLSHGCRIGYSSPQTLADQSSKIKKGSGKGDTSMLKPTLMAAVPEIMDRIYKNVM
5 NKVSEMSSFQRNLFILAYNYKMEQISKGRNTPLCDSFVFRKVRSLGGNIRLLLCG
GAPLSATTQRFMNICFCCPVGQGYGLTESAGAGTISEVWDYNTGRVGAPLVCCEI
KLKNWEEGGYFNTEKPHPRGEILIGGQSVTMGYKNEAKTKADFSSEDENGQRWL
CTGDIGEFEPDGCLKIIDRKKDLVKLQAGEYVSLGKVEAALKNLPLVDNICAYANS
YHSYVIGFVVPNQKELTELARKKGLKGTWEELCNSCEMENEVLKVLSEAAISASL
10 EKFEIPVKIRLSPEPWTPETGLVTD AFKLRKELKTHYQADIERMYGRK

SEQID No:109 (FACL4)

MKLKLNVLTIILLPVHLLITTY SALIFIPWYFLTNAKKKNAMAKRIKAKPTSDKPGSP
YRSVTHFDSLAVIDIPGADTLDKLFDHAVSKFGKKDSLGTREILSEENEMQPNGKV
15 FKKLILGNYKWMNYLEVNRVNNFGSGLTALGLKPKNTIAIFCETRAEWMIAAQ
CFKYNFPLVTLYATLGKEAVVHGLNESEASYLITSVELLESKLKTALLDISCVKHII
YVDNKAINKAEYPEGFEIHSMQSVEELGSNPENLGIPPSRPTPSDMAIVMYTSGSTG
RPKGVMHHSNLIAGMTGQCERIPGLPKDTYIGYLPLAHVLELTAEISCFTYGCR
IGYSSPLTSDQSSKIKKGSGKGDCTVLKPTLMAAVPEIMDRIYKNVMSKVQEMNYI
20 QKTLFKIGYDYKLEQIKKGYDAPLCNLLLFKKVKALLGGNVRMMLSGGAPLSPQT
HRFMNVCFCCPIGQGYGLTESCGAGTVTEVTDYTTGRVGAPLICCEIKLDWQEG
GYTINDKPNPRGEIVIGGQNISMGYFKNEEKTAEDYSVDENGQRWFCTGDIGEFHP
DGCLQIIDRKKDLVKLQAGEYVSLGKVEAALKNCPLIDNICAFKSDQSYVISFVV
PNQKRLTLLAQKQGVGEGTWVDICNNPAMEAEILKEIREAANAMKLERFEIPIKVRL
25 SPEPWTPETGLVTD AFKLRKELRNHYLKDIERMYGGK

SEQID No:110 (KIAA0095)

MDTEGFGELLQQAELAAETEGISELPHVERN LQEIQQAGERLRSRTLRTSQETA
DVKASVLLGSRGLDISHISQRLESLSAATTFEPLPVKDTDIQGFLKNEKDNALLSAI
30 EESRKRTFGMAEEYHRESMLVEWEQVKQRILHTLLASGEDALDFTQESEPSYISDV
GPPGRSSLDNIEMAYARQIYTYNEKIVNGHLQPNLVDLCASVAELDDKSISDMWT
MVKQMTDVLLTPATDALKNRSSVEVRMEFVRQALAYLEQSYKNYTLVTVFGNL

HQAQLGGVPGTYQLVRSFLNKLPAPLPGLQDGEVEGHPVWALIYYCMRCGDLLA
ASQVVNRAQHQLGEFKTWFEYMNSKDRRLSPATENKLRLHYRRALRNNTDPY
KRAVYCIIGRCDVTDNQSEVADKTEDYLWLKLNQVCFDDDGTSPPQDRLTLSQFQ
KQLLEDYGESHTVNQQPFLYFQVLFLTAQFEAAVAFLFRMERLRCHAVHVALVL
5 FELKLLKSSGQSAQLLSHEPGDPPCLRRLLNFVRLMLYTRKFESTDPREALQYFY
FLRDEKDSQGENMFLRCVSELVIESREFDMILGKLENDGSRKPGVIDKFTSDTKPII
NKVASVAENKGLFEEAAKLYDLAKNADKVLELMNKLLSPVVPQISAPQSNKERL
KNMALSIAERYRAQGISANKFVDSTFYLLLDLITFFDEYHSGHIDRAFDIERLKLVP
LNQESVEERVAAFRNFSDEIRHNLSEVLLATMNILFTQFKRLKGTSPSSSSSRPQRVIE
10 DRDSQLRSQARTLITFAGMIPYRTSGDTNARLVQMEVLMN

SEQID No:111 (KIAA0922)

MLLVLECVLFSVAQGYFRMDSSATQFHIETHENTSGLWSIWYRNHFDRSVVLNDV
FLSKETKHKMLKILNFTGPLFLPPGCWNIFSLKLA VKDIAINLFTNVFLTNTNIGAIFAIP
15 LQIYSAPTKEGSLGFEVIAHCGMHYFMGKSKAGNPWNWNGSLSLDQSTWNVDSEL
ANKLYERWKKYKNGDVCKRNVLGTTTRFAHLKKSKESESFVFFLPRLIAEPGLMLN
FSATALRSRMIKYFVVQNPSSWPVSLQLLPLSLYPKPEALVHLLHRWFGTDMQMI
NFTTGEFQLTEACPYLGTHSEESRFGILHLHLQPLEMKRVGVVFTPADYGKVTSLIL
IRNNLTVIDMIGVEGFGARELLKVGGRLPAGGSLRFKVPESTLMDCRRQLKDSK
20 QILSITKNFKVENIGPLPITVSSLKINGYNCCQGYGFEVLDCHQFSLDPNTSRDISIVFT
PDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLLPLCADVVPGPSWEESFWRLTV
FFVSLSLLGVILIAFQQAQYILMEFMKTRQRQNASSSSQQNNGPMDVISPHSYKSN
CKNFLDTYGPSDKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYS
KHKTSTAAASSTTTTEEKQTSPLGSSLPAAKEDICTDAMRENWISLRYASGINVNL
25 QKNLTLPKNLLNKEENTLKNNTIVFSNPSSECSMKEGIQTCMFPKETDIKTSENTAEF
KERELCPLKTSKKLPENHLPRNSPQYHQPDLPESISRKNNNGNNQQVPVKNEVDHCE
NLKKVDTKPSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNLQNL
NWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELSSDINVRSWCIQESTR
EVCKADAEIASSLPAAQREAEGYYQKPEKKCVDFKFCSDSSSDCGSSSGSVRASRGS
30 WGSWSSTSSSDGDKKPMVDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTV
NSLPQYAEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLENGVPCVI
QESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAPFEENMNYANGFPCPADVQT

DFIDHNSQSTWNTPPNMPAAWGHASFSSPPYLTSTRSLSPMSGFLFGSIWAPQSDV
YENCCPINPTTEHSTHMENQAVVCKEYYPGFNPFRAYMNLDIWTTTANRNNANFPL
SRDSSYCGNV

5 SEQ ID No:112 (PAS domain containing serine/threonine kinase)

MEDGGLTAFEEDQRCLSQSLPLPVSAEGPAAQTAEPSRSFSSAHRHLSRRNGLSR
LCQSR TALSEDWSSYCLSSLAAQNICTSKLHCPAAPEHTDPSEPRGSVSCCSLLRG
LSSGWSSPLLPAVPCNPKNKAFTVDAKTTEILVANDKACGLLGYSSQDLIGQKLTQ
FFLRSDSDVVEALSEEHMEADGHAAVVFQTVVDIISRSGEKIPVSVWMKMRQER
10 RLCCVVVLEPVERVSTWVAFQSDGTVTSCDSLFAHLHGYVSGEDVAGQHITDLIPS
VQLPPSGQHIPKNLKIQRSVGRARDGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRA
SVWVFCTISGLITLLPDGTIHGINSFALTLFGYGKTELLGKNITFLIPGFYSYMDLA
YNSSLQLPDLASCLDVGNESGCGERTLDPWQGQDPAEGGQDPRINVVLAGGHV
PRDEIRKLMEQDIFTGTQTELIAGGQLLSCLSPQAPGVNDVPEGSLPVHGEQALP
15 KDQQITALGREEPVAIESPGQDLLGESRSEPVDVKPFASCEDSEAPVPAEDGGSDA
GMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQLAGGSLLMHCPCYGS
EWGLWWRSDLAPSPSGMAGLSFGTPTLDEPWLGVENREELQTC LIKEQLS
LAGALDVPHAELVPTQCQAVTAPVSSCDLGGRDLCGGCTGSSSACYALATDLP
LEAVEAQEVDVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLA
20 VGSDDPDV
GSLQEQQGSCVLDDRELLLLLTGTCVDLGQGRRFRESCVGHDPTEPLEVCLV
SSEHY
AASDRESPGHVPSTLDAGPEDTCPSAEPRNLNVQVTSTPVIVMRGAAGLQ
REIQEG
AYSGSCHHRDGLRLSIQFEVRRVELQGPTPLFCCWLVKDLLHSQRDSAAR
TRLFLA
SLPGSTHSTAELTGPSLVEVLRARPWFEEPPKAVELEGLAACEGEYSQKY
STMSP
LGSGAFGFVWTAVDKEKNKEVVVKFIKKEKVLEDCWIEDPKLGKVTLEIA
ILSRV
25 EHANIIVLDIFENQGGFQLVMEKHGSGLDLFAFIDRHPRLDEPLASYIFRQ
LVSAV
GYLRLKDIHRDIKDENVIAEDFTIKLIDFGSAA YLERGKLFYTFCGTIEY
CAPEVL
MGNPYRGPELEMWSLGVTLTYTLVFEENPFCELEETVEAAIHPPYLVSKE
LMSLVSG
LLQPVPERRTTLEKLVTDPWVTQPVNLADYTWEEVCRVKNKPESGVL
SAASLEMG
NRSLSDDVAQAQELCGGPVPGAPNGQGCLHPGDPRLITS

30

SEQID No:114 (homolog of yeast golgi membrane protein yif1p (yif1p-interacting factor))
HPAGLAAAAAGTPRLPSKRRIPVSQPGMADPHQLFDDTSSAQSRGYGAQRAPGGL

SYPAASPTPHAAFLADPVSNMAMAYGSSSLAAQGKELVDKNIDRFIPITKLKYYFA
VDTMYVGRKLGLLFFPYLHQDWEVQYQQDTPVAPRFDVNAPDLYIPAMAFITYV
LVAGLALGTQDRFSPDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVA
FLGYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLKILADAAAEG
5 VPVRGARNQLRMYLTMAVAAAQPMLMYWLTFLVR

SEQ ID No:114 (Integral membrane transporter protein)

MVNYAWAGRSQRKLWWRSAVLTCCKSVVRPGYRGGLQARRSTLLKTCARARA
TAPGAMKMVAPWTRFYNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADP
10 DQYNFSSSELGGDFEFMDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFC
YQIFDFALNMLVAITVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLILLFISIL
TFKGYLISCVWNCYRYINGRNSSDVLVYVTSNDTTFVLLPPYDDATVNGAAKEPPP
PYVSA

15 SEQID No:115 (GPR49)

MDTSRLGVLLSLPVLLQLATGGSSPRSGVLLRGCPHCHCEPDGRMLLRVDCSDL
GLSELPSNLSVFTSYLDLSMNNISQLLPNPLPSLRFLEELRLAGNALTYPKGAFTGL
YSLKVLMLQNNQLRHVPTEALQNLRSLSLRLDANHISYVPPSCFSGHSLRHLW
LDDNALTEIPVQAFRSLSALQAMTLALNKIHHIPDYAFGNLSSLVVLHLHNNRIHSL
20 GKKCFDGLHSLETLDLNYNNLDEFPTAIRTLNLKELGFHSNNIRSIPEKAFVGNPS
LITHFYDNPIQFVGRSAFQHLPELRTLTLNGASQITEFPDLTGANLESILTGAQIS
SLPQTVCNQLPNLQVLDLSYNLLEDLPSFSVCQKLQKIDLRHNEIYEIKVDTFQQL
SLRSLNLAWNKIAIHPNAFSTLPSLIKLDLSSNLLSFPITGLHGLTHLKLGTGNHAL
QSLISSENFPELKVIEMPYAYQCCAFGVCENAYKISNQWNKGDNSSMDDLHKKDA
25 GMFQAQDERDLEDFLDFFEDLKALHSVQCSPSPGPKPCEHLLDGWLIRIGVWTI
AVLALTCNALVTSTVFRSPLYISPIKLLIGVIAAVNMLTGVSVAVLAVDAFTFGSF
ARHGAWWENGVGCHVIGFLSIFASESSVFLTLAALERGFSVKYSAKFETKAPFSS
LKVIIIICALLALTMAAVPLLGGSKYGASPLCLPLPFGEPTMGYMVALILLNSLCF
LMMTIAYTKLYCNLDKGDLENWDSCSMVKHIALLLFTNCILNCPVAFLSFSSLINLT
30 FISPEVIKFILLVVVPLPACLNPLLYILFNPHFKEDLVSLRKQTYVWTRSKHPSLMSI
NSDDVEKQSCDSTQALVTFTSSSITYDLPPSSVPSAPYPTESCHLSSVAFVPCL

SEQ ID No:116 (NAP-1 related protein/NAP-1-like protein)

KEQSELDQDLDDVEEVEEEETGEETKLKARQLTVQMMQNPQILAALQERLDGLV
ETPTGYIESLPRVVKRRVNALKNLQVKCAQIEAKFYEEVHDLERKYAVLYQPLFD
KRFEIINAIYEPTEEECWKPDEEDEISEELKEKAKIEDEKKDEEKEDPKGIPEFWLT
5 VFKNVDLLSDMVQEHDEPILKHLKDIKVKFSDAGQPMFVLEFHFEPNEYFTNEVL
TKTYRMRSEPDSDPFSFDGPEIMGCTGCQIDWKKGKNVTLKTIKKKQKHKGRT
VRTVTKTVSNDFFNFAPPEVIPKFSAFDDDAEAILAADFEIGHFLRERIIPRSVLYF
TGEAIEDDDDDYDEEGEEADEGYQLFEEVKSCSKLFQRWLQ

10 SEQID No:117 (SPTLC2)

MRPEPGGCCCRRTVRANGCVANGEVRNGYVRSSAAAAAAAAAAGQIHVTONGG
LYKRPFNEAFEETPMLVAVLTYVGYGVLTFLGYLRDFLRYWRIEKCHHATEREEQ
KDFVSLYQDFENFYTRNLYMRIRDNWNRPICSVPGARVDIMERQSHDYNWSFKY
TGNIKGVINMGSYNYLGFARNTGSCQEAATAKVLEEYAGVCSTRQEIGNLDKHE
15 ELEELVARFLGVEAAMA YGMGFATNSMNIPALVGKGCLILSDELNHASLVLGARL
SGATIRIFKHNNMQSLEKLLKDAIVYGQPRTRRPWKKILILVEGIYSMEGSIVRLPE
VIALKKKYKAYLYLDEAHSIGALGPTGRGVVEYFGLDPEDVDVMMGTFTKSFGA
SGGYIGGKKELIDYLRTHSHSAVYATSLSPVVEQIITSMKCMGQDGTSLGKECV
QQLAENTRYFRRLKEMGFIIYGNEDSPVPLMLYMPAKIGAFGREMLKRNIGVV
20 VVGFPATPIESRARFCLSAHTKEILD TALKEIDEVGDLLQLKYSRHRLVPLDRPF
DETTYEETED

SEQID No:118 (Delta-like homolog)

MTATEALLRVLLLLLAFGHSTYGAECFPACNPQNGFCEDDNVCRCQPGWQGPLC
25 DQCVTSPGCLHGLCGEPGQCICTDGWDGELCDRDVRACSSAPCANNGTCVSLDG
GLYECSCAPGYSGKDCQKKDGPCVINGSPCQHGGTCVDDEGRASHASCLCPPGFS
GNFCEIVANSCTPNPCENDGVCTDIGGDFRCRCPAGFIDKTCRPTVNCASSPCQN
GGTCLQHTQVSYECLCKPEFTGLTCVKKRALSPQQVTRLPSGYGLAYRLTPGVHE
LPVQQPEHRILKVSMKELNKKTPLLTEGQAICFTILGVLTSLVVLGTVGIVFLNKCE
30 TWVSNLRYNHMLRKKKNLLQYNSGEDLA VNIIFPEKIDMTTFSKEAGDEEI

SEQ ID No: 119 (25 kDa microsomal signal peptidase subunit)

MAAAAVQGGRRSGGSGGCSGAGGASNCGTGSGRSGLLDKWKIDDKPVKIDKWDG
SAVKNSLDDSAKKVLLEKYKYVENFGLIDGRLTICTISCFFAIVALIWDYMHFPFES
KPVLAALCVISYFVMMGILTIYTSYKEKSIFLVAHRKDPTGMDPDDIWQLSSSLKRF
DDKYTLKLTFISGR TKQQREAEFTKSI AKFFDHSGTLVMDA YEPEISRLHDSLAIER
5 KIK

SEQ ID No: 120 (APP-C99)

MDAEFRHDSGYEVHHQKLVFFAEDVGSNKGAIIGLMVGGVVIATVIVITLVMLKK
KQYTSIHG VVEVDAAVTPEERHLSKMQQNGYENPTYKFFEQMQN
10

SEQ ID No: 121 (Psen-2)

MLTFMASDSEEEVCDERTSLMSAESPTPRSCQEGRQGPEDGENTAQWRSQENEED
GEEDPDRYVCSGVPGRPPGLEEELTKYGAKHVIMLFVPVTLCMIVVATIKSVRF
YTEKNGQLIYTPFTEDTPSVGQRLNSVLNTLMISVIVVMTIFLVVLYKYRCYKFI
15 HGWLMSSLMLLFLFTYIYLGEVLKTYNVAMDYPTLLLT VWNFGAVGMVCIHWK
GPLVLQQA YLMISALMALVFIKYLPEWSAWVILGAISVYDLVAVLCPKGPLRML
VETAQERNEPIFALIYSSAMVWTVGMAKLDPSSQ GALQLPYDPMEEDSYDSFG
EPSYPEVFEPPLTGYPGEELEEEEEERG VKLGLGDFIFYSVLVGKAAATGSGDWNTT
LACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIFYFSTDNLVRPFMDTLASHQL
20 YI

SEQ ID No: 122 (FADS1)

MGTRAARPAG LPCGAENPAR RRLALGARQQ IHSWSPRTPS TRLTAPAGPA
RGVARPAMAP DPVAAETA AQ GTPRYFTWD EVAQRSGCEE RWLVIDRKVY
25 NISEFTRRHP GGSRVISHYA GQDATDPFVA FHINKGLVKK YMNSLLIGEL
SPEQPSLEPT KNKELTDEFR ELRATVERMG LMKANHVFFL LYLLHILLLE
GAAWLT LWVF GTSFLPFLC AVLLSAVQAQ AGWLQHDFGH LSVFSTSKWN
HLLHHFVIGH LKGAPASWWS HMHFQHHAKP NCFRKDPDIN MHPFFFALGK
ILSVELGKQK KKYMPYNHQH KYFFLIGPPA LLPLYFQWYI FYFVIQRKKW
30 VDLAWMITFY VRFFLT YVPL LGLKAFLGLF FIVRFLESNW FVWVTQMNI
PMHIDHDRNM DWVSTQLQAT CNVHKSAFND WFSGHLNFQI EHHLFPTMPR
HNYHKVAPLV QSLCAKHGIE YQSKPLLSAF ADIHSCLKES GQLWLDAYLH Q

SEQ ID No: 123 (DEGS)

MGSRVSREDF EWVYTDQPHA DRRREILAKY PEIKSLMKPD PNLIWIIMM
VLTQLGAFYI VKDLWDKWVI FGAYAFGSCI NHSMTLAIHE IAHNAAFGNC
5 KAMWNRWFGM FANLPIGIPY SISFKRYHMD HHRYLGADGV DVDIPTDFEG
WFFCTAFRKF IWVILQPLFY AFRPLFINPK PITYLEVINT VAQVTFDILI
YYFLGIKSLV YMLAASLLGL GLHPISGHFI AEHYMFLKGH ETYSYYGPLN
LLTFNVGYHN EHHDFPNIPG KSLPLVRKIA AEYYDNLPHY NSWIKVLYDF
VMDDTISPYS RMKRHQKGEM VLE

10

SEQ ID No: 124 (SCD4/ HYPOTHETICAL PROTEIN FLJ21032)

MPGPATDAGK IPFCDAKEEI RAGLESSEGG GGPFRPGARG QRQNIVWRNV
VLMSLLHLGA VYSLVLIPKA KPLTLLWAYF CLLLAALGVT AGAHLRWSHR
SYRAKLPLRI FLAVANSMAF QNDIFERSRD HRAHHKYSET DADPHNARRG
15 FFFSHIGWLF VRKHRDVIEK GRKLDVTDLL ADPVVRIQRN TQHIQKEGRA
LNQEAACEML REWHQGHILK VTLPLGLHILA LLHTHCNHSE KCCLMLRALS
VSLEVF

SEQ ID No: 125 (FADS3)

20 MGGVGEPGPR EGPAQPGAPL PTFCWEQIRA HDQPGDKWL V IERRVYDISR
WAQRHPGGSR LIGHHGAEDA TDAFRAFHQD LNFVRKFLQP LLIGELAPEE
PSQDGPLNAQ LVEDFRALHQ AAEDMKLFDA SPTFFAFLLG HILAMEVLAW
LLIYLLGPGW VPSALAAFIL AISQAQSWCL QHDLGHASIF KKSWWNHVAQ
KFVMGQLKGF SAHWWNFRHF QHHAKPNIFH KDPDVTVAPV FLLGESSVEY
25 GKKKRRYLPY NQQHLYFFLI GPPLTLVNF EVENLAYMLV CMQWADLLWA
ASFYARFFLS YLPFYGVPGV LLFFVAVRVL ESHWFWWITQ MNHIPKEIGH
EKHRDWVSSQ LAATCNVEPS LFTNWFSGHL NFQIEHHLFP RMPRHNYSRV
APLVKSLCAK HGLSYEVKPF LTALVDIVRS LKKSGDIWLD AYLHQ

30

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(75) Inventor/Applicant (for US only): HOPF, Carsten
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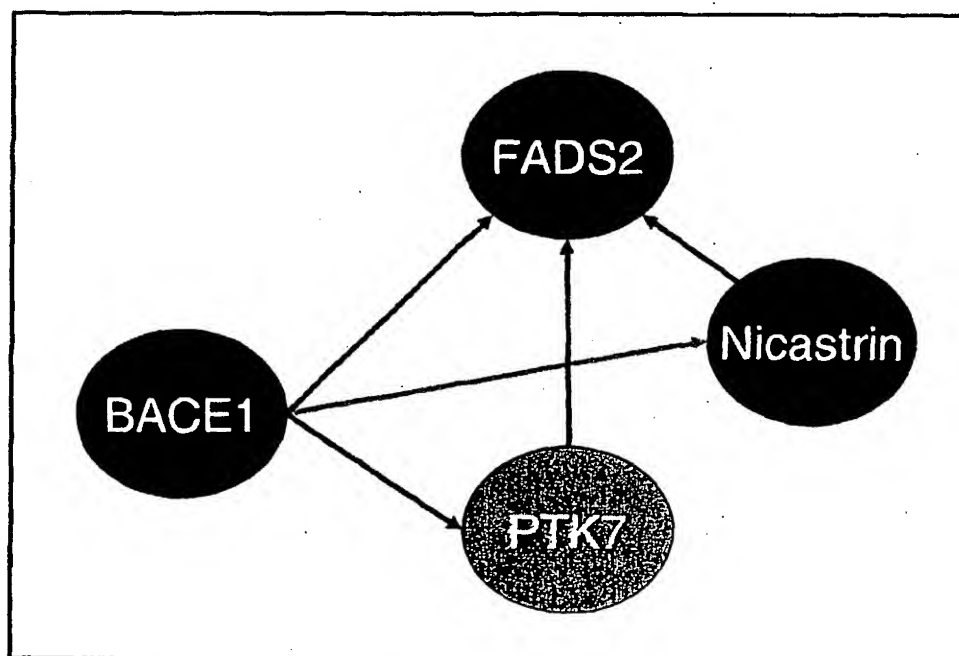
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(54) Title: TREATMENT OF NEURODEGENERATIVE DISEASES



(57) Abstract: The present invention relates to the uses of FADS2 interacting molecules, especially FADS2 inhibitors, for the preparation of a medicament for the treatment of neurodegenerative diseases, specially Alzheimer's disease.

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B. FIELDS SEARCHED

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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EP0-Internal, BIOSIS, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01/70993 A (SCOTIA HOLDINGS PLC; WINTHER, MICHAEL, DAVID; SMITH, HEIDI, LYNN; ALLE) 27 September 2001 (2001-09-27) the whole document	1-6,19, 20,38-40
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>CHO H P ET AL: "Cloning, expression, and nutritional regulation of the mammalian Delta-6 desaturase" JOURNAL OF BIOLOGICAL CHEMISTRY, AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD, US, vol. 274, no. 1, 1999, pages 471-477, XP002111713 ISSN: 0021-9258 the whole document</p> <p>-----</p>	
A	<p>WO 00/58473 A (CURAGEN CORPORATION; SHIMKETS, RICHARD, A; LEACH, MARTIN) 5 October 2000 (2000-10-05) * see ORF1574, SEQ.ID's 3147 & 3148 * page 75, line 16</p> <p>-----</p>	
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A	<p>WO 01/62897 A (VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE VZW; ANNAERT, W) 30 August 2001 (2001-08-30) the whole document</p> <p>-----</p>	
T	<p>HOPF C ET AL: "Discovery of new therapeutic targets by integrated protein pathway and chemical proteomic analysis of APP processing." SOCIETY FOR NEUROSCIENCE ABSTRACT VIEWER AND ITINERARY PLANNER, vol. 2003, 2003, pages Abstract No. 406.5 URL-http://sf, XP002322663 & 33RD ANNUAL MEETING OF THE SOCIETY OF NEUROSCIENCE; NEW ORLEANS, LA, USA; NOVEMBER 08-12, 2003 the whole document</p> <p>-----</p>	

INTERNATIONAL SEARCH REPORT

Information on patent family members

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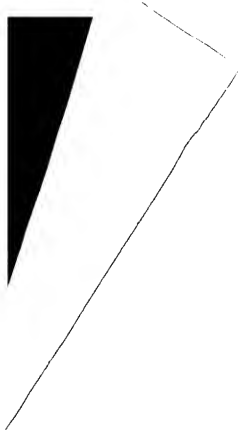
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